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Figures

Figure 1.

1 AAAATGTATG GATACAACTT ACGTTTGATG AAAGATTGG GCTTGAAGAC CCAGAAGATG
TTTTACATAC CTATGTTGAA TGCAAACCTAC TTTCTAAACC CGAACTTCTG GGTCTTCTAC

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TGTATACGTT CATACTAAAA CATCTTCAAC TCCTTGGGTC ACTACCTTGA TATAATCCCG

121 GCTGGTGTGG TTCTGGTACT GTACCAGGAA AACAGATTTC TAAAGGAAAT CAAATTAGGA
CGACCACACC AAGACCATGA CATGGTCCTT TTGTCTAAAG ATTCCTTTA GTTAAATCCT

+1 MetAsn IlePheLeu LeuAsnLeuLeu ThrGluGlu ValArgLeu
]-----

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ATTCTAAACA TAGACTACTT ATAAAAGGAA GACTTGAAG ATTGTCTCCT CCATTCTAAT

+1 TyrSerCysThr ProArgAsn PheSerVal SerIleArgGlu GluLeuLys ArgThrAsp

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ATGTCGACGT GTGGAGCATT GAAGAGTCAC AGGTATTCCC TTCTTGATTT CTCTTGGCTA

+1 ThrIlePheTrp ProGlyCys LeuLeuVal LysArgCysGly GlyAsnCys AlaCysCys

301 ACCATTTTCT GGCCAGGTTG TCTCCTGGTT AAACGCTGTG GTGGGAAGTG TGCTGTGTGT
TGTTAAAGA CCGGTCCAAC AGAGGACCAA TTTGCGACAC CACCTTGAC ACGGACAACA

+1 LeuHisAsnCys AsnGluCys GlnCysVal ProSerLysVal ThrLysLys TyrHisGlu

361 CTCCACAATT GCAATGAATG TCAATGTGTC CCAAGCAAAG TTAATAAAA ATACCACGAG
GAGGTGTTAA CGTTACTTAC AGTTACACAG GGTTCGTTTC AATGATTTT TATGGTGTCT

+1 ValLeuGlnLeu ArgProLys ThrGlyVal ArgGlyLeuHis LysSerLeu ThrAspVal

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CAGGAAGTCA ACTCTGTTTT CTGGCCACAG TCCCCTAAGG TGTTTAGTGA GTGGCTGCAC

+1 AlaLeuGluHis HisGluGlu CysAspCys ValCysArgGly SerThrGly Gly
----->

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CGGGACCTCG TGGTACTCCT CACACTGACA CACACGTCTC CTCGTGTCC TCCTATCGGC

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GTAGTGGTGG TCGTCGAGAA CGGGTCTCGA CACGTCACGT CACCGACTAA GATAATCTCT

601 ACGTATGCGT TATCTCCATC CTTAATCTCA GTTGTGTTGCT TCAAGGACCT TTCATCTTCA
TGCATACGCA ATAGAGGTAG GAATTAGAGT CAACAAACGA AGTTCCTGGA AAGTAGAAGT

661 GGATTTACAG TGCATTCTGA AAGAGGAGAC ATCAAACAGA ATTAGGAGTT GTGCAACAGC
CCTAAATGTC ACGTAAGACT TTCTCCTCTG TAGTTTGTCT TAATCCTCAA CACGTTGTGC

567227 "498450

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AGAAAACTCT CCTCCGGATT TCCTGCTCTC TTTCCAGAA GTTAGCACCT TTCTTTTAAT

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TGACACGTTT ACTCGTGGAC TAAGGCAACG GAACGAATTG AGATTTTCAG GTACAGGACC

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CGGATTTTAG CATATTTTAG ACCTAAAAAA AAAAAAAAAA ACGAGTATAA GTGTATACAT

1021 AACCAGAACA TTCTATGTAC TACAAACCTG GTTTTTAAAA AGGAACATAG TTGCTATGAA
TTGGTCTTGT AAGATACATG ATGTTTGGAC CAAAAATTTT TCCTTGATAC AACGATACTT

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1141 TGCCATTTAG AAGAAGAGAA CTACATTCAT GGTTTGGAAG AGATAAACCT GAAAAGAAGA
ACGGTAAATC TTCTTCTCTT GATGTAAGTA CCAAACCTTC TCTATTTGGA CTTTTCTTCT

1201 GTGGCCTTAT CTTCACTTTA TCGATAAGTC AGTTTATTG TTTCAATTG TACATTTTA
CACCAGAAATA GAAGTGAAAT AGCTATTGAG TCAAATAAAC AAGTAACAC ATGTAAAAAT

1261 TATTCTCCTT TTGACATTAT AACTGTTGGC TTTTCTAATC TTGTTAAATA TATCTATTTT
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1321 TACCAAGGT ATTTAATATT CTTTTTATG ACAACTTAGA TCACTATTT TTAGCTGGT
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1381 AAATTTTCT AAACACAATT GTTATAGCCA GAGGAACAAA GATGATATAA AATATTGTTG
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1441 CTCTGACAAA AATACATGTA TTCAATCTC GTATGGTGCT AGAGTTAGAT TAATCTGCAT
GAGACTGTTT TTATGTACAT AAGTAAGAG CATACCAGCA TCTCAATCTA ATTAGACGTA

1501 TTTAAAAAC TGAATTGGAA TAGAATTGGT AAGTTGCAAA GACTTTTTGA AAATAATTAA
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1561 ATTATCATAT CTTCCATTCC TGTTATTGGA GATGAAAATA AAAAGCAACT TATGAAAGTA
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1621 GACATTCAGA TCCAGCCATT ACTAACCTAT TCCTTTTTTG GGGATCTG AGCCTAGCTC
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1681 AGAAAAATCAT AAGCACCTT GAAAAAGACT TGGCAGCTTC CTGATAAAGC GTGCTGTGCT
TCITTTTGTA TTTCGTGGAA CTTTTTCTGA ACCGTCGAAG GACTATTTTC CACGACACGA

1741 GTGCAGTAGG AACACATCCT ATTTATTGTG ATGTTGTGGT TTTATTATCT TAACTCTGT
CACGTCATCC TTGTGTAGGA TAAATAACAC TACAACACCA AAATAATAGA ATTTGAGACA

1801 TCCATACACT TGTATAATA CATGGATATT TTTATGTACA GAAGTATGTC TCTTAACCA
AGGTATGGA ACATATTTAT GTACCTATAA AAATACATGT CTTCATACAG AGAATTGGTC

Fig. 1 (cont.)

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1861 TTCACTTATT GTACCTGG
AAGTGAATAA CATGGACC

Fig. 1 (cont.)

Figure 2. Predicted VEGF-like protein encoded by Incyte contig of 8/12/98

1 MNIFLLNLLT EEVRLYSCTP RNFSVSIREE LKRTDTIFWP GCLLVKRCGG
51 NCACCLHNCN ECQCVPSKVT KKYHEVLQLR PKTGVRGLHK SLTDVALEHH
101 EECDCVCRGS TGG

65 49 24 7 4 9 2 3 4 5 6

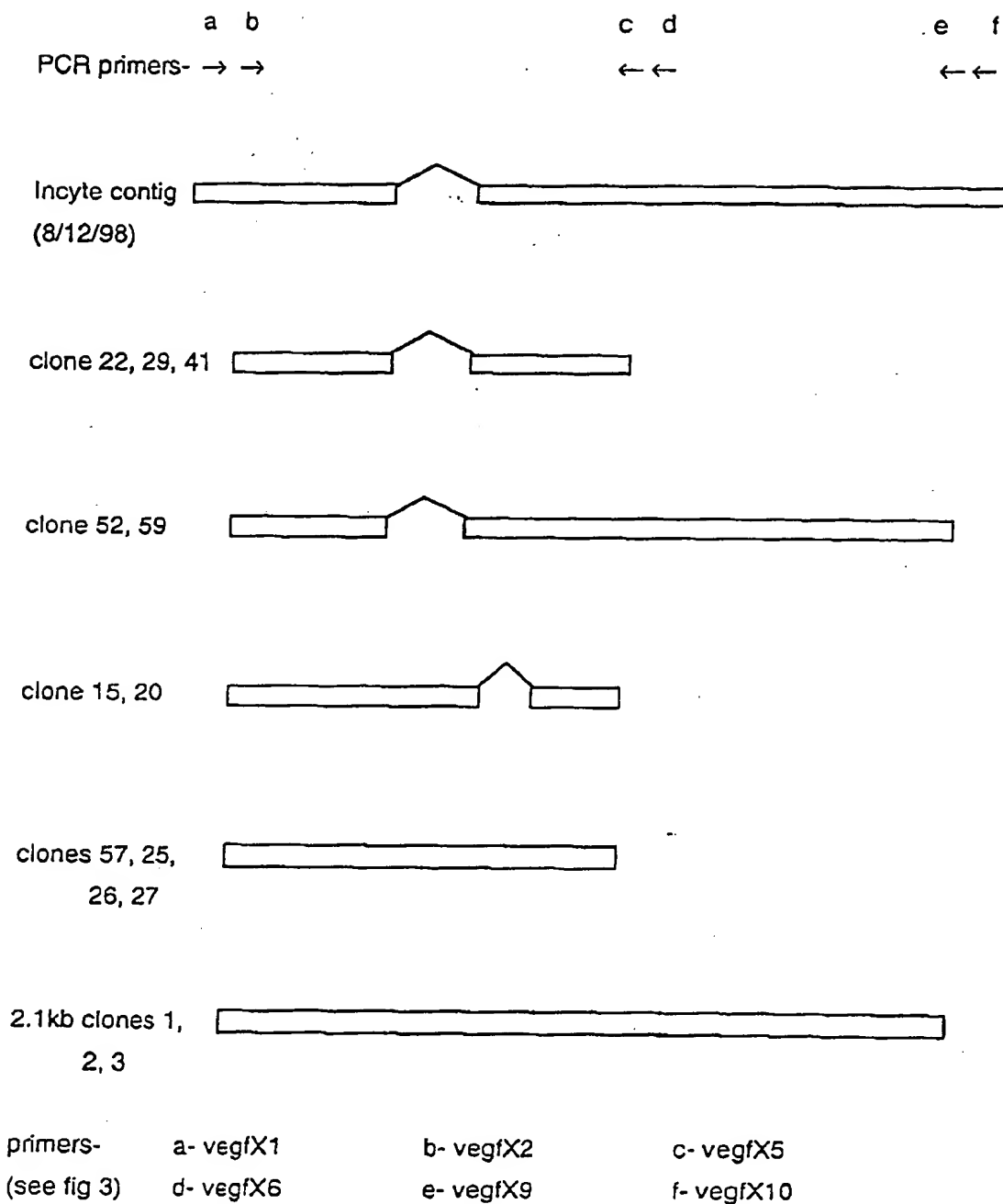
Express Mail Label No.
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Figure 3. PCR primers for cloning VEGF-X

vegfx1	AAAATGTATGGATACAACTTAC
vegfx2	GTTTGATGAAAGATTGGGCTTG
vegfx3	TTTCTAAAGGAAATCAAATTAG
vegfx4	GATAAGATTGTATCTGATG
vegfx5	GATGTCTCCTCTTTCAG
vegfx6	GCACAACTCCTAATTCTG
vegfx7	AGCACCTGATTCCGTTGC
vegfx8	TAGTACATAGAATGTTCTGG
vegfx9	AAGAGACATACTTCTGTAC
vegfx10	CCAGGTACAATAAGTGAAGTGA

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Figure 4. Variants Isolated by PCR



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Figure 5. VEGF-X 5' RACE primers

vegX11	CCTTAGAAATCTGTTTTCTGGTACAG
vegX12	GGAAAATATTCATCAGATACAAATCTTATCC
vegX13	GGTCCAGTGGCAAAGCTGAAGG
vegX14	CTGGTTCAAGATATCGAATAAGGTCTTCC

66727 499460

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Figure 6. DNA sequence assembled from in-house clones and 5'RACE

1 TGCCAGAGCA GGTGGGCGCT TCCACCCAG TGCAGCCTTC CCCTGGCGGT GGTGAAAGAG
ACGGTCTCGT CCACCCGCGA AGGTGGGCTC ACCTCGGAAG GGGACCGCCA CCACTTTCTC

61 ACTCGGGAGT CGCTGCTTCC AAAGTGCCCG CCGTGAGTGA GCTCTCACCC CAGTCAGCCA
TGAGCCCTCA GCGACGAAGG TTTCACGGGC GGCACCTACT CGAGAGTGGG GTCAGTCGGT

+2 MetSerLeu PheGlyLeuLeu LeuLeuThr SerAlaLeu AlaGlyGlnArg GlnGlyTh
]-----

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TTACTCGGAG AAGCCCGAAG AGGACGACTG TAGACGGGAC CGGCCGGTCT CTGTCCCTG

+2 rGlnAlaGlu SerAsnLeuSer SerLysPhe GlnPheSer SerAsnLysGlu GlnAsnGln

181 TCAGGCGGAA TCCAACCTGA GTAGTAAATT CCAGTTTTC AGCAACAAGG AACAGAACGG
AGTCCGCCTT AGGTTGGACT CATCATTTAA GGTCAAAGG TCGTTGTTCC TTGTCTTGCC

+2 yValGlnAsp ProGlnHisGlu ArgIleIle ThrValSer ThrAsnGlySer IleHisSe

241 AGTACAAGAT CCTCAGCATG AGAGAAATTAT TACTGTGTCT ACTAATGGAA GTATTACACG
TCATGTTCTA GGAGTCGTAC TCTCTAATA ATGACACAGA TGATTACCTT CATAAGTGTC

+2 rProArgPhe ProHisThrTyr ProArgAsn ThrValLeu ValTrpArgLeu ValAlaVa

301 CCCAAGGTTT CCTCATACTT ATCCAAGAAA TACGGTCTTG GTATGGAGAT TAGTAGCAGT
GGGTTCCAAA GGAGTATGAA TAGGTTCTTT ATGCCAGAAC CATACCTCTA ATCATCGTCA

+2 lGluGlnAsn ValTrpIleGln LeuThrPhe AspGluArg PheGlyLeuGlu AspProGln

361 AGAGGAAAAT GTATGGATAC AACTTACGTT TGATGAAAGA TTTGGGCTTG AAGACCCAGA
TCTCCTTTTA CATACCTATG TTGAATGCAA ACTACTTTCT AAACCCGAAC TTCTGGGTCT

+2 uAspAspIle CysLysTyrAsp PheValGlu ValGluGlu ProSerAspGly ThrIleLe

421 AGATGACATA TGCAAGTATG ATTTTGTAGA AGTTGAGGAA CCCAGTGATG GAACTATATT
TCTACTGTAT ACGTTCATAC TAAACATCT TCAACTCCTT GGGTCACTAC CTTGATATAA

+2 uGlyAspTrp CysGlySerGly ThrValPro GlyLysGln IleSerLysGly AsnGlnIl

481 AGGGCGCTGG TGTGGTCTG GTACTGTACC AGGAAAACAG ATTTCTAAAG GAAATCAAAT
TCCCGCGACC ACACCAAGAC CATGACATGG TCCTTTTGTG TAAAGATTTC CTTTAGTTTA

+2 eArgIleArg PheValSerAsp GluTyrPhe ProSerGlu ProGlyPheCys IleHisTy

541 TAGGATAGA TTTGTATCTG ATGAATATTT TCCTTCTGAA CCAGGGTCT GCATCCACTA
ATCCTATTCT AAACATAGAC TACTTATAAA AGGAAGACTT GGTCCCAAGA CGTAGGTGAT

+2 rAsnIleVal MetProGlnPhe ThrGluAla ValSerPro SerValLeuPro ProSerAl

601 CAACATCTTC ATGCCACAAT TCACAGAAGC TGTGAGTCCT TCAGTGCTAC CCCCTTCAGC
GTGTAAACG TACGGTGTTA AGTGTCTTCG AACTCAGGA AGTCACGATG GGGGAAGTCC

+2 aLeuProLeu AspLeuLeuAsn AsnAlaIle ThrAlaPhe SerThrLeuGlu AspLeuIl

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Fig. 6 (cont)

661 TTGCGCACTG GACCTGCTTA ATAATGCTAT AACTGCCTTT AGTACCTTGG AAGACCTTAT
AAACGGTGAC CTGGACGAAT TATTACGATA TTGACGGAAA TCATGGAACC TTCTGGAATA

+2 eArgTyrLeu GluProGluArg TrpGlnLeu AspLeuGlu AspLeuTyrArg ProThrTr

721 TCGATATCTT GAACCAGAGA GATGGCAGTT GGACTTAGAA GATCTATATA GGCCAACTTG
AGCTATAGAA CTGGTCTCT CTACCGTCAA CCTGAATCTT CTAGATATAT CCGGTTGAAC

+2 pGlnLeuLeu GlyLysAlaPhe ValPheGly ArgLysSer ArgValValAsp LeuAsnLe

781 GCAACTTCTT GGCAAGGCTT TTGTTTTTGG AAGAAAATCC AGAGTGGTGG ATCTGAACCT
CGTTGAAGAA CCGTTCCGAA AACAAAAACC TTCTTTTAGG TCTCACCACC TAGACTTGGA

+2 uLeuThrGlu GluValArgLeu TyrSerCys ThrProArg AsnPheSerVal SerIleAr

841 TCTAACAGAG GAGGTAAGAT TATACAGCTG CACACCTCGT AACTTCTCAG TGTCCATAAG
AGATTGTCTC CTCCATTCTA ATATGTCGAC GTGTGGAGCA TGAAGAGTC ACAGGTATTC

+2 gGluGluLeu LysArgThrAsp ThrIlePhe TrpProGly CysLeuLeuVal LysArgCy

901 GGAAGAACTA AAGAGAACCG ATACCATTTT CTGGCCAGGT TGTCTCCTGG TTAAACGCTG
CCTTCTTGAT TTCTCTTGGC TATGGTAAAA GACCGGTCCA ACAGAGGACC AATTGCGAC

+2 sGlyGlyAsn CysAlaCysCys LeuHisAsn CysAsnGlu CysGlnCysVal ProSerLy

961 TGGTGGGAAC TGTGCCTGTT GTCTCCACAA TTGCAATGAA TGTCAATGTG TCCCAAGCAA
ACCACCCTTG ACACCGACAA CAGAGGTGTT AACGTTACTT ACAGTTACAC AGGGTTCGTT

+2 sValThrLys LysTyrHisGlu ValLeuGln LeuArgPro LysThrGlyVal ArgGlyLe

1021 AGTTACTAAA AAATACCACG AGGTCTCTCA GTTGAGACCA AAGACCGGTG TCAGGGGATT
TCAATGATTT TTTATGGTGC TCCAGGAAGT CAACTCTGGT TTCTGGCCAC AGTCCCCTAA

+2 uHisLysSer LeuThrAspVal AlaLeuGlu HisHisGlu GluCysAspCys ValCysAr

1081 GCACAAATCA CTCACCGACG TGGCCCTGGA GCACCATGAG GAGTGTGACT GTGTGTGACG
CGTGTTTAGT GAGTGGCTGC ACCGGGACCT CGTGTACTC CTCACACTGA CACACACGTC

+2 gGlySerThr GlyGly
----->

1141 AGGGAGCACA GGAGGATAGC CGCATCACCA CCAGCAGCTC TTGCCAGAG CTGTGCAGTG
TCCCTCGTGT CCTCCTATCG GCGTAGTGGT GGTCTGTCGAG AACGGGTCTC GACACGTCAC

1201 CAGTGGCTGA TTCTATTAGA GAACGTATGC GTTATCTCCA TCCTTAATCT CAGTTGTTTG
GTCACCGACT AAGATAATCT CTGCATACG CAATAGAGGT AGGAATTAGA GTCAACAAAC

1261 CTTCAGGAC CTTTCATCTT CAGGATTAC AGTGCATTCT GAAAGAGGAG ACATCAAACA
GAAGTTCCTG GAAAGTAGAA GTCCTAAATG TCACGTAAGA CTTTCTCCTC TGTAGTTTGT

1321 GAATTAGGAG TTGTGCAACA GCTCTTTTGA GAGGAGGCCT AAAGGACAGG AGAAAAGGTC
CTTAATCCTC AACACGTTGT CGAGAAAACCT CTCCTCCGGA TTTCTGTCC TCTTTTCCAG

1381 TTCAATCCTG GAAAGAAAAT TAAATGTTGT ATTAAATAGA TCACCAGCTA GTTTCAGAGT
AAGTTAGCAC CTTTCTTTTA ATTTACAACA TAATTTATCT AGTGGTCCAT CAAAGTCTCA

1441 TACCATGTAC GTATTCCACT AGCTGGGTTT TGTATTTTCT TTCTTTTCAT ACGGCTTAGG

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1. *Phragmites australis* (Cav.) Trin. ex Steud.
 2. *Scirpus americanus* L.
 3. *Spartina patens* (Muhl.) B. & P.
 4. *Distichlis spicata* (L.) Nees
 5. *Eleocharis acicularis* (L.) Rostk Schmidt
 6. *Eleocharis obtusa* (L.) Nees
 7. *Eleocharis tenuis* (L.) Rostk Schmidt
 8. *Eleocharis palustris* (L.) Rostk Schmidt
 9. *Eleocharis acicularis* (L.) Rostk Schmidt
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 18. *Eleocharis obtusa* (L.) Nees
 19. *Eleocharis tenuis* (L.) Rostk Schmidt
 20. *Eleocharis palustris* (L.) Rostk Schmidt
 21. *Eleocharis acicularis* (L.) Rostk Schmidt
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 26. *Eleocharis obtusa* (L.) Nees
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 38. *Eleocharis obtusa* (L.) Nees
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 41. *Eleocharis acicularis* (L.) Rostk Schmidt
 42. *Eleocharis obtusa* (L.) Nees
 43. *Eleocharis tenuis* (L.) Rostk Schmidt
 44. *Eleocharis palustris* (L.) Rostk Schmidt
 45. *Eleocharis acicularis* (L.) Rostk Schmidt
 46. *Eleocharis obtusa* (L.) Nees
 47. *Eleocharis tenuis* (L.) Rostk Schmidt
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 49. *Eleocharis acicularis* (L.) Rostk Schmidt
 50. *Eleocharis obtusa* (L.) Nees
 51. *Eleocharis tenuis* (L.) Rostk Schmidt
 52. *Eleocharis palustris* (L.) Rostk Schmidt
 53. *Eleocharis acicularis* (L.) Rostk Schmidt
 54. *Eleocharis obtusa* (L.) Nees
 55. *Eleocharis tenuis* (L.) Rostk Schmidt
 56. *Eleocharis palustris* (L.) Rostk Schmidt
 57. *Eleocharis acicularis* (L.) Rostk Schmidt
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 62. *Eleocharis obtusa* (L.) Nees
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 66. *Eleocharis obtusa* (L.) Nees
 67. *Eleocharis tenuis* (L.) Rostk Schmidt
 68. *Eleocharis palustris* (L.) Rostk Schmidt
 69. *Eleocharis acicularis* (L.) Rostk Schmidt
 70. *Eleocharis obtusa* (L.) Nees
 71. *Eleocharis tenuis* (L.) Rostk Schmidt
 72. *Eleocharis palustris* (L.) Rostk Schmidt
 73. *Eleocharis acicularis* (L.) Rostk Schmidt
 74. *Eleocharis obtusa* (L.) Nees
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 97. *Eleocharis acicularis* (L.) Rostk Schmidt
 98. *Eleocharis obtusa* (L.) Nees
 99. *Eleocharis tenuis* (L.) Rostk Schmidt
 100. *Eleocharis palustris* (L.) Rostk Schmidt

10

Figure 7. New Sequence + Incyte ESTs

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TAAACAAATT TGGAACCCCTT TGACCAAGTC CAGGTCCAAA ACGAAACTAG GAAAAGTTTT

61 ACTGGAGACA CAGAAGAGGG CTTCTAGGAA AAAGTTTTGG GATGGGATTA TGTGGAACT
TGACCTCTGT GTCTTCTCCC GAAGATCCTT TTTCAAAACC CTACCCTAAT ACACCTTTGA

121 ACCCTGCGAT TCTCTGCTGC CAGAGCAGGC TCGGCGCTTC CACCCAGTG CAGCCTTCCC
TGGGACGCTA AGAGACGACG GTCTCGTCCG AGCCGCGAAG GTGGGGTCAC GTCGGAAGGG

181 CTGGCGGTGG TGAAAGAGAC TCGGGAGTCG CTGCTTCCAA AGTGCCCCGC GTGAGTGAGC
GACCGCCACC ACTTTCTCTG AGCCCTCAGC GACGAAGGTT TCACGGGCGG CACTCACTCG

+2 Met SerLeuPhe GlyLeuLeu LeuLeuThrSer AlaLeuAl
|-----

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+2 aGlyGlnArg GlnGlyThrGln AlaGluSer AsnLeuSer SerLysPheGln PheSerSe

301 CGGCCAGAGA CAGGGGACTC AGGCGGAATC CAACCTGAST AGTAAATTCC AGTTTTCCAG
GCCGGTCTCT GTCCCCTGAG TCCGCCTTAG GTTGGACTCA TCATTTAAGG TCAAAAGGTC

+2 rAsnLysGlu GlnTyrGlyVal GlnAspPro GlnHisGlu ArgIleIleThr ValSerTh

361 CAACAAGGAA CAGTACGGAG TACAAGATCC TCAGCATGAG AGAATTATTA CTGTGTCTAC
GTTGTTCTCT GTCATGCCTC ATGTTCTAGG AGTCGTACTC TCTTAATAAT GACACAGATG

+2 rAsnGlySer IleHisSerPro ArgPhePro HisThrTyr ProArgAsnThr ValLeuVa

421 TAATGGAGT ATTCACAGCC CAAGGTTTCC TCATACTTAT CCAAGAAATA CGGTCTTGGT
ATTACCTTCA TAAGTGTCGG GTTCCAAAGG AGTATGAATA GGTCTTTTAT GCCAGAACCA

+2 lTrpArgLeu ValAlaValGlu GluAsnVal TrpIleGln LeuThrPheAsp GluArgPh

481 ATGGAGATTA GTAGCAGTAG AGGAAAATGT ATGGATACAA CTACGTTTG ATGAAAGATT
TACCTCTAAT CATCGTCATC TCCTTTTACA TACCTATGTT GAATGCAAAC TACTTTCTAA

+2 eGlyLeuGlu AspProGluAsp AspIleCys LysTyrAsp PheValGluVal GluGluPr

541 TGGGCTTGA GACCCAGAAG ATGACATATG CAAGTATGAT TTTGTAGAAG TTGAGGAACC
ACCCGAACCT CTGGGTCTTC TACTGTATAC GTTCATACTA AAACATCTTC AACTCCTTGG

+2 oSerAspGly ThrIleLeuGly ArgTrpCys GlySerGly ThrValProGly LysGlnIl

601 CAGTGATGGA ACTATATTAG GCGCTGGTG TGTTCTGGT ACTGTACCAG GAAACAGAT
GTCACTACCT TGATATAATC CCGCGACCAC ACCAAGACCA TGACATGGTC CTTTTGTCTA

+2 eSerLysGly AsnGlnIleArg IleArgPhe ValSerAsp GluTyrPhePro SerGluPr

661 TTCTAAAGGA AATCAAATTA GGATAAGATT TGTATCTGAT GAATATTTTC CTTCTGAACC
AAGATTTCTT TAGTTTAAT CCTATTCTAA ACATACACTA CTTATAAAGS GAAGACTTGG

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Fig. 7 (cont.)

+2 oGlyPheCys IleHisTyrAsn IleValMet ProGlnPhe ThrGluAlaVal SerProSe

721 AGGGTTCTGC ATCCACTACA ACATTGTCAT GCCACAATTC ACAGAAGCTG TGAGTCCTTC
TCCCAAGACG TAGGTGATGT TGTAACAGTA CGGTGTTAAG TGTCTTCGAC ACTCAGGAAG

+2 rValLeuPro ProSerAlaLeu ProLeuAsp LeuLeuAsn AsnAlaIleThr AlaPheSe

781 AGTGCTACCC CCTTCAGCTT TGCCACTGGA CCTGCTTAAT AATGCTATAA CTGCCTTTAG
TCACGATGGG GGAAGTCGAA ACGGTGACCT GGACGAATTA TTACGATATT GACGGAAATC

+2 rThrLeuGlu AspLeuIleArg TyrLeuGlu ProGluArg TrpGlnLeuAsp LeuGluAs

841 TACCTTGGAA GACCTTATTC GATATCTTGA ACCAGAGAGA TGGCAGTTGG ACTTAGAAGA
ATGGAACCTT CTGGAATAAG CTATAGAACT TGGTCTCTCT ACCGTCAACC TGAATCTTCT

+2 pLeuTyrArg ProThrTrpGln LeuLeuGly LysAlaPhe ValPheGlyArg LysSerAr

901 TCTATAAGG CCAACTTGGC AACTTCTTGG CAAGGCTTTT GTTTTGGAA GAAATCCAG
AGATATATCC GGTGAACCG TTGAAGAACC GTTCCGAAA CAAAACCTT CTTTATAGTC

+2 gValValAsp LeuAsnLeuLeu ThrGluGlu ValArgLeu TyrSerCysThr ProArgAs

961 AGTGCTGGAT CTGAACCTTC TAACAGAGGA GGTAAGATTA TACAGCTGCA CACCTCGTAA
TCACCACCTA GACTTGAAG ATTGTCTCTT CCATTCTAAT ATGTCGACGT GTGGAGCATT

+2 nPheSerVal SerIleArgGlu GluLeuLys ArgThrAsp ThrIlePheTrp ProGlyCy

1021 CTTCTCAGTG TCCATAAGGG AAGAACTAAA GAGAACCGAT ACCATTTTCT GGCCAGGTTG
GAAGAGTCAC AGGTATTCCC TTCTTGATT CTCTGGCTA TGGTAAAAGA CCGGTCCAAC

+2 sLeuLeuVal LysArgCysGly GlyAsnCys AlaCysCys LeuHisAsnCys AsnGluCy

1081 TCTCCTGGTT AAACGCTGTG GTGGGAACCTG TGCTGTGTT CTCCACAATT GCAATGAATG
AGAGGACCAA TTTGCGACAC CACCCTTGAC ACGGACAACA GAGGTGTAA CGTTACTTAC

+2 sGlnCysVal ProSerLysVal ThrLysLys TyrHisGlu ValLeuGlnLeu ArgProLy

1141 TCAATGTGTC CCAAGCAAAG TTAATAAAAA ATACCACGAG GTCCTTCAGT TGAGACCAAA
ASTTACACAG GGTTCGTTTC AATGATTTTT TATGGTGCTC CAGGAAGTCA ACTCTGGTTT

+2 sThrGlyVal ArgGlyLeuHis LysSerLeu ThrAspVal AlaLeuGluHis HisGluGl

1201 GACCGGTGTC AGGGGATTGC ACAAATCACT CACCGACGTG GCCCTGGAGC ACCATGAGGA
CTGGCCACAG TCCCCTAACG TGTTTAGTGA GTGGCTGCAC CGGGACCTCG TGGTACTCCT

+2 uCysAspCys ValCysArgGly SerThrGly Gly
----->
1261 GTGTGACTGT GTGTGCAGAG GGAGCACAGG AGGATAGCCG CATCACCACC AGCAGCTCTT
CACACTGACA CACACGTCTC CCTCGTGTC TCCTATCGGC GTAGTGGTGG TCGTCGAGAA

1321 GCCCAGACCT GTGCAGTGCA GTGGCTGATT CTATTAGAGA ACGTATGCGT TATCTCCATC
CGGGTCTTGA CACGTCACGT CACCGACTAA GATAATCTCT TGCATACGCA ATAGAGGTAG

1381 CTTAATCTCA GTTGTGTTGCT TCAAGGACCT TTCATCTTCA GGATTTACAG TGCATTCTGA
GAATTAGAGT CAACAAACGA AGTTCCTGGA AAGTAGAAGT CCTAATGTC ACGTAAGACT

Fig. 7 (cont.)

1441 AAGAGGAGAC ATCAAACAGA ATTAGGAGTT GTGCAACAGC TCTTTTGAGA GGAGGCGTAA
TTCTCCTCTG TAGTTTGTCT TAATCCTCAA CACGTTGTCT AGAAAACTCT CCTCCGGATT

1501 AGGACAGGAG AAAAGGTCTT CAATCGTGA AAGAAAATTA AATGTTGTAT TAAATAGATC
TCCTGTCCTC TTTTCCAGAA GTTAGCACCT TTCTTTTAAT TTACAACATA ATTTATCTAG

1561 ACCAGCTAST TTCAGAGTTA CCATGTACGT ATTCCACTAG CTGGGTTCTG TATTTCACTT
TGGTCGATCA AAGTCTCAAT GGTACATGCA TAAGGTGATC GACCCAAGAC ATAAAGTCAA

1621 CTTTCGATAC GGCTTAGGGT AATGTCAGTA CAGGAAAAAA ACTGTGCAAG TGAGCACCTG
GAAAGCTATG CCGAATCCCA TTACAGTCAT GTCCTTTTTT TGACACGTC ACTCGTGGAC

1691 ATTCCGTTGC CTTGGCTTAA CTCTAAAGCT CCATGTCCTG GGCCTAAAT CGTATAAAT
TAAGGCAACG GAACCGAATT GAGATTTTCA GGTACAGGAC CCGGATTTTA GCATATTTTA

1741 CTGGATTTTT TTTTTTTTTT TGGCGCATAT TCACATATGT AAACCAGAAC ATTCTATGTA
GACCTAAAAA AAAAAAAAAA AACGCGTATA AGTGATACA TTTGGTCTTG TAAGATACAT

1801 CTACAAACCT GGTTTTTAAA AAGGAACATAT GTTGCTATGA ATTAACTTG TGTCATGCTG
GATGTTTGA CCAAAAATTT TCCCTTGATA CAACGATACT TAATTTGAAC ACAGTACGAC

1861 ATAGGACAGA CTGGATTTTT CATATTTCTT ATTAAATTT CTGCCATTTA GAAGAAGAGA
TATCCTGCT GACCTAAAAA GTATAAAGAA TAATTTTAAA GACGGTAAAT CTTCTCTCT

1921 ACTACATTCA TGGTTTGGAA GAGATAAACC TGAAAAGAAG AGTGGCCTTA TCTTCACTTT
TGATGTAAGT ACCAAACCTT CTCTATTGG ACTTTTCTTC TCACCGGAAT AGAAGTGAAA

1981 ATCGATAAGT CAGTTTATTT GTTTCATTGT GTACATTTTT ATATTCTCCT TTTGACATTA
TAGCTATCA GTCAATAAAA CAAAGTAACA CATGTAAAAA TATAAGAGGA AAACGTGAAT

2041 TAACTGTTGG CTTTCTAAT CTGTAAAT ATATCTATTT TTACCAAAGG TATTTAATAT
ATTGACAACC GAAAAGATTA GAACAATTTA TATAGATAAA AATGGTTTCC ATAAATTATA

2101 TCTTTTTTAT GACAACTTAG ATCAACTATT TTTAGCTTGG TAAATTTTTC TAAACACAAT
AGAAAAATA CTGTTGAATC TAGTTGATAA AAATCGAACC ATTTAAAAAG ATTTGTGTTA

2161 TGTTATASCC AGAGGAACAA AGATGATATA AAATATTGTT GCTCTGACAA AAATACATGT
ACAATATCGG TCTCCTTGTT TCTACTATAT TTTATAACAA CGAGACTGTT TTTATGTACA

2221 ATTTCACTCT CGTATGGTGC TAGAGTTAGA TTAATCTGCA TTTTAAAAAA CTGAATTGGA
TAAAGTAAGA GCATACCACG ATCTCAATCT AATTAGACGT AAAATTTTTT GACTTAACCT

2281 ATAGAATTGG TAAGTTGCAA AGACTTTTTG AAAATAATTA AATTATCATA TCTTCCATTC
TATCTTAACC ATTCAACGTT TCTGAAAAAC TTTTATTAAT TTAATAGTAT AGAAGGTAAG

2341 CTGTTATTGG AGATGAAAAT AAAAGCAAC TTATGAAAGT AGACATTGAG ATCCAGCCAT
GACAATAACC TCTACTTTTA TTTTTCGTTG AATACTTTCA TCTGTAAGTC TAGGTCGGTA

2401 TACTAACCTA TTCCTTTTTT GGGGAAATCT GAGCCTAGCT CAGAAAAACA TAAAGCACCT
ATGATTGGAT AAGGAAAAAA CCCCTTTAGA CTCGGATCGA GTCTTTTTGT ATTTCTGGA

2461 TGAAAAAAGC TTGGCAGCTT CCTGATAAAG CGTGCTGTGC TGTGCACTAG GAACACATCC
ACTTTTTCTG AACCGTCGAA GGACTATTC GCACGACACG ACACGTCATC CTTGTGTAGG

2521 TATTTATGTT GATGTTGTGG TTTTATTATC TTAAGCTCTG TTCCATACAC TTGTATAAAT
ATAAATAACA CTACAACACC AAAATAATAG AATTTGAGAC AAGGTATGTG AACATATTTA

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Fig. 7. (cont.)

2581 ACATGGATAT TTTTATGTAC AGAAGTATGT CTCTTAACCA GTTCACTTAT TGTACTCTGG
TGTACCTATA AAAATACATG TCTTCATACA GAGAATTGGT CAAGTGAATA ACATGAGACC

2641 CAATTTAAAA GAAAATCAGT AAAATATTTT GCTTGTAATA TGCTTAATAT CGTGCCTAGG
GTTAAATTTT CTTTATGTC TTTTATAATA CGAACATTTT ACGAATTATA GCACGGATCC

2701 TTATGTGGTG ACTATTTGAA TCAAAAATGT ATTGAATCAT CAAATAAAG AATGTGGCTA
AATACACCAC TGATAAACTT AGTTTTTACA TAACTTAGTA GTTATTTTC TTACACCGAT

2761 TTTTGGGGAG AAAATT
AAAACCCCTC TTATA

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Figure 8. Additional oligonucleotides used for amplification of entire coding region

5'-1	TTTGTTTAAACCTTGGGAAACTGG
5'-2	GTCCAGGTTTTGCTTTGATCC

65 70 75 80 85 90 95 100

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Figure 9. DNA Sequence Of Clones 4 & 7, Identical Clones Containing The Entire Open Reading Frame

```

1  TTTGTTTAAA CCTTGGGAAA CTGGTTCAGG TCCAGGTTTT GCTTTGATCC TTTTCAAAAA
   AAACAAATTT GGAACCCCTT GACCAAGTCC AGGTCCAAAA CGAAACTAGG AAAAGTTTTT

61  CTGGAGACAC AGAAGAGGGC TCTAGGAAAA AGTTTTGGAT GGGATTATGT GGAAACTACC
   GACCTCTGTG TCTTCTCCCG AGATCCTTTT TCAAAACCTA CCCTAATACA CCTTTGATGG

121 CTGCGATTCT CTGCTGCCAG AGCAGGCTCG GCGCTTCCAC CCCAGTGCAG CCTTCCCCTG
   GACGCTAAGA GACGACGGTC TCGTCCGAGC CGCGAAGGTG GGGTCACGTC GGAAGGGGAC

181 GCGGTGGTGA AAGAGACTCG GGAGTCGCTG CTTCCAAAGT GCCCGCCGTG ACTGAGCTCT
   CGCCACCACT TTCTCTGAGC CCTCAGCGAC GAAGGTTTCA CGGGCGGCAC TCACTCGAGA

+2          MetSer LeuPheGly LeuLeuLeu LeuThrSerAla LeuAlaGl
   ]-----

241 CACCCCAAGT AGCCAAATGA GCCTCTTCGG GCTTCTCCTG CTGACATCTG CCCTGGCCGG
   GTGGGGTCAG TCGGTTTACT CGGAGAAGCC CGAAGAGGAC GACTGTAGAC GGGACCGGCC

+2 yGlnArgGln GlyThrGlnAla GluSerAsn LeuSerSer LysPheGlnPhe SerSerAs
   -----

301 CCAGAGACAG GGGACTCAGG CGGAATCCAA CCTGAGTAGT AAATTCAGT TTCCAGCAA
   GGTCTCTGTC CCCTGAGTCC GCCTTAGGTT GGACTCATCA TTTAAGGTCA AAGGTCGTT

+2 nLysGluGln AsnGlyValGln AspProGln HisGluArg IleIleThrVal SerThrAs
   -----

361 CAAGGAACAG AACGGAGTAC AAGATCCTCA GCATGAGAGA ATTATTACTG TGTCTACTAA
   GTTCCTTGTC TTGCCTCATG TTCTAGGAGT CGTACTCTCT TAATAATGAC ACAGATGATT

+2 nGlySerIle HisSerProArg PheProHis ThrTyrPro ArgAsnThrVal LeuValTr
   -----

421 TGGAAGTATT CACAGCCCAA GGTTCCTCA TACTTATCCA AGAATACGG TCTTGGTATG
   ACCTTCATAA GTGTCGGGTT CCAAAGGAGT ATGAATAGGT TCTTTATGCC AGAACCATAC

+2 pArgLeuVal AlaValGluGlu AsnValTrp IleGlnLeu ThrPheAspGlu ArgPheGl
   -----

481 GAGATTACTA GCAGTAGAGG AAAATGTATG GATACAACTT ACGTTTGATG AAAGATTGG
   CTCTAATCAT CGTCATCTCC TTTTACATAC CTATGTTGAA TGCAAACTAC TTTCTAAACC

+2 yLeuGluAsp ProGluAspAsp IleCysLys TyrAspPhe ValGluValGlu GluProSe
   -----

541 GCTTGAAGAC CCAGAAGATG ACATATGCAA STATGATTTT GTAGAAGTTG AGGAACCCAG
   CGAACTTCTG GGTCTTCTAC TGTATACGTT CATACTAAAA CATCTTCAAC TCCTTGGGTC

+2 rAspGlyThr IleLeuGlyArg TrpCysGly SerGlyThr ValProGlyLys GlnIleSe
   -----

601 TGATGGAAct ATATTAGGGC CTTGGTGTGG TTCTGGTACT GTACCAGGAA AACAGATTTC
   ACTACCTTGA TATAATCCCG CGACCACACC AAGACCATGA CATGGTCCTT TTGTCTAAAG

+2 rLysGlyAsn GlnIleArgIle ArgPheVal SerAspGlu TyrPheProSer GluProGl
   -----

661 TAAAGGAAAT CAAATTAGCA TAAGATTGTG ATCTGATGAA TATTTTCCTT CTGAACCAGG

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Fig. 9 (cont.)

ATTTCTTTTA GTTTAATCCT ATTCTAAACA TAGACTACTT ATAAAAGGAA GACTTGGTGC
 +2 yPheCysIle HisTyrAsnIle ValMetPro GlnPheThr GluAlaValSer ProSerVa

 721 GTTCTGCATC CACTACAACA TTGTCATGCC ACAATTCACA GAAGCTGTGA GTCCTTCAGT
 CAAGACGTAG GTGATGTTGT AACAGTACGG TGTTAAGTGT CTTCGACACT CAGGAAGTCA
 +2 lLeuProPro SerAlaLeuPro LeuAspLeu LeuAsnAsn AlaIleThrAla PheSerTh

 781 GCTACCCCTC TCAGCTTTGC CACTGGACCT GCTTAATAAT GCTATAACTG CCTTAGTAC
 CGATGGGGGA AGTCGAAACG GTGACCTGGA CGAATTATTA CGATATTGAC GGAATCATG
 +2 rLeuGluAsp LeuIleArgTyr LeuGluPro GluArgTrp GlnLeuAspLeu GluAspLe

 841 CTTGGAAGAC CTTATTCGAT ATCTTGAACC AGAGAGATGG CAGTTGGACT TAGAAGATCT
 GAACCTTCTG GAATAAGCTA TAGAAGCTGG TCTCTCTACC GTCAACCTGA ATCTCTCTAG
 +2 uTyrArgPro ThrTrpGlnLeu LeuGlyLys AlaPheVal PheGlyArgLys SerArgVa

 901 ATATAGGCCA ACTTGGCAAC TTCTTGGCAA GGCTTTTGTT TTTGGAAGAA AATCCAGAGT
 TATATCCGGT TGAACCGTTG AAGAACCGTT CCGAAACAA AAACCTTCTT TTAGGTCTCA
 +2 lValAspLeu AsnLeuLeuThr GluGluVal ArgLeuTyr SerCysThrPro ArgAsnPh

 961 GGTGGATCTG AACCTTCTAA CAGAGGAGGT AAGATTATAC AGCTGCACAC CTCGTAACCT
 CCACCTAGAC TTGGAAGATT GTCTCCTCCA TTCTAATATG TCGACGTGTG GAGCATTGAA
 +2 eSerValSer IleArgGluGlu LeuLysArg ThrAspThr IlePheTrpPro GlyCysLe

 1021 CTCAGTGTC ATAAGGGAAG AACTAAAGAG AACCGATACC ATTTTCTGGC CAGGTTGTCT
 GAGTCACAGG TATTCCTTC TTGATTCTC TTGGCTATGG TAAAAGACCG GTCCAACAGA
 +2 uLeuValLys ArgCysGlyGly AsnCysAla CysCysLeu HisAsnCysAsn GluCysGl

 1081 CCTGGTAAA CGCTGTGGTG GGAAGTGTG CTGTTGTCTC CACAATTGCA ATGAATGTCA
 GGACCAATTT GCGACACCAC CCTTGACAGG GACAACAGAG GTGTTACGT TACTTACGT
 +2 nCysValPro SerLysValThr LysLysTyr HisGluVal LeuGlnLeuArg ProLysTh

 1141 ATGTGTCCCA AGCAAAGTTA CTAATAATA CCACGAGGTC CTTCAGTTGA GACCAAAGAC
 TACACAGGCT TCGTTTCAAT GATTTTTTAT GGTGCTCCAG GAAGTCAACT CTGGTTTCTG
 +2 rGlyValArg GlyLeuHisLys SerLeuThr AspValAla LeuGluHisHis GluGluCy

 1201 CGGTGTCCAG GGATTGCACA AATCACTCAC CGACGTGGCC CTGGAGCACC ATGAGGAGTG
 GCCACAGTCC CCTAACGTGT TTAGTGAGTG GCTGCACCGG GACCTCGTGG TACTCCTCAC
 +2 sAspCysVal CysArgGlySer ThrGlyGly
 ----->
 1261 TGACTGTGTC TGCAGAGGGA GCACAGGAGG ATAGCCGCAT CACCACCAGC AGCTCTTGCC
 ACTGACACAC ACGTCTCCCT CGTGTCTCTC TATCGGCGTA GTGGTGCTCG TCGAGAACGG
 1321 CAGAGCTGTC CAGTGCAGTG GCTGATTCTA TTAGAGAACG TATGCGTTAT CTCCATCCTT
 GTCTCGACAC GTCACGTCAC CGACTAAGAT AATCTCTTGC ATACGCAATA GAGGTAGGAA
 1381 AATCTCAGTT GTTTGCTTCA AGGACCTTTC ATCTTCAGGA TTTACAGTGC ATTCTGAAAG

Fig. 9 (cont.)

TTAGAGTCAA CAAACGAAGT TCCTGGAAG TAGAAGTCCT AAATGTCACG TAAGACTTTC

1441 AGGAGACATC AAACAGAATT AGGAGTTGTG CAA
TCCTCTGTAG TTTGTCTTAA TCCTCAACAC GTT

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Figure 10. Predicted Full-length Polypeptide Sequence

1 MSLFGLLLT SALAGQRQGT QAESNLSSKF QFSSNKEQYG VQDPQHERII
51 TVSTNGSIHS PRFPHTYPRN TVLVWRLVAV EENVWIQLTF DERFGLEDPE
101 DDICKYDFVE VEEPSDGTIL GRWCGSGTVF GKQISKGNQI RIRFVSDEYF
151 PSEPGFCIHY NIVMPQFTEA VSPSVLPESA LPLDLLNNAI TAFSTLEDLI
201 RYLEPERWQL DLEDLYRPTW QLLGKAFVFG RKSRVVDLNL LTEEVRLYSC
251 TPRNFSVSIR EELKRTDTIF WPGCLLVKRC GGNCACCLHN CNECQCVPSK
301 VTKKYHEVLQ LRPKTGVRGL HKSLTDVALE HHEECDCVCR GSTGG

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Figure 11 Alignment of VEGF-X with Other VEGFs

```

      .           20           .           40           .           60
VEGF_HUMAN : .....
PLGF_HUMAN : .....
VEGB_HUMAN : .....
VEGC_HUMAN : .....
VEGD_HUMAN : .....
990126vegX : MSLEFLLLLTSALAGQRQGTQAESNLSSKQFSSNKEQNCVQDPQHERIITVSTNGSINSPRFPHTYF : 6

      .           80           .           100          .           120
VEGF_HUMAN : .....
PLGF_HUMAN : .....
VEGB_HUMAN : .....
VEGC_HUMAN : .....
VEGD_HUMAN : .....
990126vegX : RNTVLVWRLLVAVEZNVWILQTFDSRFGLDPEDDICKYDFVEV--EEPDDGTILGRWCGSGTVPCXK : 13

      140          .           160          .           180          .           200
VEGF_HUMAN : .....
PLGF_HUMAN : .....
VEGB_HUMAN : .....
VEGC_HUMAN : ALLPSPREAPAAAAAFESGLDLSDAEPDAGZATAYASKDLEEQLRSVSSVDELMTVLVPEYWKHKYKCC : 8
VEGD_HUMAN : ---MYREWVVVNVFMHLYVQLVQCSSNEHGPVKRSSQSTLERSEQQIRAAASLELLRITHSEDKL : 6
990126vegX : SKGNQIRIRFVSDEYFPSEPGPCIHYNIVMPQFTEAVSPSVLPSPALPLDLLNNAITAFSTLEDLIRY : 20

      .           220          .           240          .           260
VEGF_HUMAN : WVENSLAFLYLHAKNSGAAPMAEGGCONHHKFFQ-VGAYNHITLDGFCYPDSEIYI : 73
PLGF_HUMAN : FPCFLQLACLAAPAVPPEWALSAGNCSSEVPPQE-VGAYNHITLDGFCYPDSEIYI : 73
VEGB_HUMAN : SPLRLRLAALALAPAPAPVSQPDAPGHQKRSW-VGAYNHITLDGFCYPDSEIYI : 69
VEGC_HUMAN : LRKQWQHNREQANLNSRTEETIKFAAAHYNTKSNV-NVATQCHVVPVTVLNGTVAKC : 15
VEGD_HUMAN : WRCLRLKSTSTDSRSASHSTRFAATFYDITKVVDEEKGQSSTETCEASLCKXTNTF : 17
990126vegX : LEPERWQECLEDEYRPTWLLGKAPVFCRKSRYVQLNLTTEVLYSCFPANFVSIRILKATDTI : 27

      280          .           300          .           320          .           340
VEGF_HUMAN : K...P...M...ND...Y...E...N...R...PHQG...Q...G...L...K... : 131
PLGF_HUMAN : S...S...L...CD...N...H...VETAN...K...RSGDR...P...S...Y...VR... : 131
VEGB_HUMAN : V...S...C...PD...DG...E...G...QH...M...H...Y...S...Q...E...S... : 129
VEGC_HUMAN : K...P...S...Y...NS...G...N...ST...Y...K...T...FE...V...P...L...S... : 212
VEGD_HUMAN : K...U...H...F...NE...S...H...I...N...ST...Y...K...T...FE...V...P...L...S... : 192
990126vegX : W...L...L...K...NCA...LHNCNECH...K...V...K...Y...H...K...Q...P...K...T...G...V...R...L...K...S...T...D...A...L...E...N...E...E... : 336

      .           360          .           380          .           400
VEGF_HUMAN : EKADBARQEKKSVRGKCKGQKRRKKKSRYKSMVSP- : 166
PLGF_HUMAN : ELDEKMKPER- : 161
VEGB_HUMAN : EKAKDSAVKPDSPR- : 139
VEGC_HUMAN : SKLIRYRIVHSIIRRLPATLPQCOAANKTCPTNYMWNHICRCLAQEDFMFSSDAGDSDTGPHD : 280
VEGD_HUMAN : RTAPRHPYSIIRRSIQIPEDRCSKSKKLCPIIDMLWDSNK-KCVLQEEENPLAGT- : 245
990126vegX : C...S...T...G... : 345

      .           420          .           440          .           460
VEGF_HUMAN : .....
PLGF_HUMAN : .....
VEGB_HUMAN : .....
VEGC_HUMAN : GPNKELDEETCQCVCRAGLAPASCGPHKELDRNSCCQCVCKNKLFPSSQCGANREFDENTCQCVCXKATCP : 348
VEGD_HUMAN : .....
990126vegX : ..... : 286

      .           480          .           500          .           520          .           540
VEGF_HUMAN : TSKC-SKNTDSRKAKRQLELNERTCQCDKPR- : 215
PLGF_HUMAN : ..... : 186
VEGB_HUMAN : TCRCRIRRSFRLRQGRGLELNPDTGRCCKLRA- : 416
VEGC_HUMAN : RNPLNPNPCACETESQXCLLKCKKFFHQTCSCYRRPCTNRQKACEPCFSYGEVCRVPSYWKRP : 354
VEGD_HUMAN : NESTFECKESLETSCQXKHLFHPCTCSCEDRCFPFTRPCASCKTACAKHCRFPKXRAAAGPHSKNP : 354
990126vegX : ..... : 354

VEGF_HUMAN : ..... : -
PLGF_HUMAN : ..... : -
VEGB_HUMAN : ..... : -
VEGC_HUMAN : CMS- : 419
VEGD_HUMAN : ..... : -
990126vegX : ..... : -

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Figure 13. Primers for Expression of VEGF-X

E.coli expression of domain-

vegX-6 AATTGGATCCGAGAGTGGTGGATCTGAACC
vegX-7 AATTGGATCCGGGAAGAAAATCCAGAGTGG
vegX-8 GGTTGAATTCATTATTTTTAGTAACTTTGCTTGGGACAC
vegX-9 AATTGAATTCATTATCCTCCTGTGCTCCCTC

Baculovirus/insect cell expression of full-length protein-

vegbac1
AATTGGATCCGGAGTCTCACCATCACCACCATCATGAATCCAACCTGAGTAGTAAATTCC
C
vegbac2 AATTGAATTCGCTATCCTCCTGTGCTCCCTCTGC

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1 >3993180H1 LUNOT003 INCYTE
2 CACAAATCACTCACCGACGCCCCCTGGAGCACCATGAGGNGTGTGACTGTGTGAGGGAGCACAGGAGGATAGCC
3 GCATCACCACCAGCAGCTCTTGCCAGAGCTGTGTCAGTGCAGTGGCTGATTCTATAGAGAACGTATGCGTTATCTCCAT
4 CCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCATCTTCAGGATTACAGTGCATTCTGAAAGAGGAGACATCAAACAG
5 AATTAGGASTTGTGCAACAGCTCTTTGAGAGGAGGCTAAAGGACAGGAGAAAGGCTT
6 >3510192H1 CONCN0T01 INCYTE
7 TGCAGTGCAGTGGCTGATTCTATAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTT
8 TCATCTTCAGGATTACAGTGCATTCTGAAAGAGGAGACATCAACAGAAATTAGGAGTTGTGCAACAGCTCTTTTGAGAG
9 GAGCCCTAAAGGACAGGAGAAAGSTCTTCAATCGTGGAAAGAAATTAATGTTGTATTAAATAGATCACCAGCTAGTT
10 TCAGAGTTACCATGTACGTATTCACCTAGCTGGGTTCTGTATT
11 >2559870H1 ADRETUT01 INCYTE
12 CACGAGGTCCTTCAGTTGAGACCAAAGACCGGTGTGAGGGGATTGCACAAATCACTCACCACGCTGGCCCTGGAGCACCA
13 TGAGGAGTGTGACTGTGTGTCAGAGGGAGCAGGGGGATAGCCGCATCACCACCGAGCTCTTGCCAGAGCTGTGC
14 ACTCCAGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCA
15 TCTTCAGGATTACAGTGCATTCTGAAAGAGGAGA
16 >3979767H1 LUNGTUT08 INCYTE
17 GAGGATAGCCGCATCACCACAGCAGCTCTTGCCAGAGCTGTGTCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGC
18 GTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCATCTTCAGGATTACAGTGCATTCTGAAAGAGGAG
19 ACATCAAAACAGAATTAGGAGTTGTGCAACAGCTCTTTTGAGAGGAGGCCCTAAAGGACAGGAGAAAAGCTCTCAATCGTG
20 GAAAGAAATTAATGTTCTATTAAATAGACACCAGCT
21 >3980011H1 LUNGTUT08 INCYTE
22 GAGGATAGCCGCATCACCACAGCAGCTCTTGCCAGAGCTGTGTCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGC
23 GTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCATCTTCAGGATTACAGTGCATTCTGAAAGAGGAGA
24 CATCAAAACAGAATTAGGAGTTGTGCAACAGCTCTTTTGAGAGGAGGCCCTAAAGGACAGGAGAAAAGCTCTCAATCGTG
25 AAAGAAAATTAAATGTTGTATTAAATAGATCACA
26 >4825396H1 BLADDT01 INCYTE
27 GAGAACCGATACCATTTCTGCGCCAGGTTGTCTCCTGGTTAAACGCTGTGGTGGGAACGTGTCCTGTTGTCTCCACAATT
28 GCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAATACCACGAGGTCCTCAGTTGAGACCAAGACCGGTGTCT
29 ACGGATTCGACAAATCACTCACCAGCTGCGCCCTCGAGCACCATGAGGAGTGTGACTGTGTGTGACAGCGGACACAGG
30 AGGATAGCCGCATCACCACCA
31 >3073703H1 BONEUNT01 INCYTE
32 AGAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTATACAGCTGCCACACCTCGTAACTTCTCAGT
33 GTCCATAAGGGAAGAATAAGAGAAACCGATACCATTTCTGCGCCAGGTTGTCTCCTGTTAAACGCTGTGGTGGGAAC
34 GTGCTGTGTCTCCACAATTGCAATGAATGTGTGTCCTCCAAAGCAAGTTACTAAAAATACCACGAGGTCCTTCAG
35 TTTGACACCAAGACCGGTGTGAGGCAATTGCAAAATCA
36 >1302516H1 PLACNOT02 INCYTE
37 AGGAAATCAAATTAGGATAAGATTGTATCTGATGAATATTTCTCTGAAACCTTCTAACAGAGGAGTAAGATTATAC
38 AGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCATTTCTGCGCCAGGTTGTCT
39 CCTGGTTAAACGCTGTGGTGGGAACTGTGCTGTGTCTCCACAATTGCAATGAATGTCAATGTGTGCCAAGCAAAGTT
40 ACTAAAAATACCACGAGGTC
41 >3684109H1 HEAANC01 INCYTE
42 ATTTCACTTTCAGGATTACAGTGCATTCTGAAANAGGAGAAATCAAAACANAATTAGGAGTTGTGCAACAGCTCTTTTGA
43 GAGGAGGCTTAAAGGACAGGAGAAAAGGCTTCAATCGTGGAAANAAATTAATGTTGTATTAAATAGATCACCAGCTA
44 GTTTCAGAGTTACCATGTACGTATTCCTAGCTGGGTTCTGTATTTCAGTTCTTTCGATACGGCTTAGGGTAATGTGAG
45 TACAGGAAAAAACTGTGCAAGTGAACCTGATTCCGTTGCTTGCCTT
46 >4713188H1 BRAHCT01 INCYTE
47 CAAAGTTACTAAAAATACCACGAGTCTCAGTTGAGACCAAGACCGGTGTGAGGGGATTGCACAAATCACTCACCAG
48 ACGTGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGTGTCAGAGGGAGCACAGGAGGATACCCGCATCACCACAGCAG
49 CTCTTGCCAGAGCTGTGTCAGTGCAGTGGCTGATTCTATTAGAGAAGCTATGCGTTATCTCCATCCTTAATCTCAGTTGT
50 TTGCT
51 >458823H1 XERANOT01 INCYTE
52 ANGAGTTGCCAGAGCTGTGTCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTT
53 GTTTGNTTCAAGGACCTTTCATCTTCAGGATTACAGTGCATTCTGAAAGAGGAGACATCAACAGAAATTAGGAGTTGTG
54 CAACACCTCTTTTGAGAGGAGGCCCTAAAGGNCAGGACAAAGCTCTTCAATCGTGGAAAGAAAATTAAATGTTGTATTAA
55 ATAGATC
56 >1303909H1 PLACNOT02 INCYTE
57 AGGAAATCAAATTAGGATAAGATTGTATCTGATGAATATTTCTCTTCTGAACCTTCTAACAGAGGAGGTAAGATTATAC
58 AGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCATTTCTGCGCCAGGTTGTCT
59 CCTGGTTAAACGCTGTGGTGGGAACTGTGCTGTGTCTCCACAATTGCAATGAATGTCAATGTGTGCCAAG
60 >2739211H1 OVARNOT09 INCYTE
61 GTGCATTCTGAAAGAGGAGACATCAAAACAGAAATTAGGAGTTGTGCAACAGCTCTTTTGAGAGGAGGCCCTAAAGGACAGGA
62 GAAAAGGCTTCAATCGTGGAAAGAAAATTAAATGTTGTATTAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACG
63 TATTCCACTAGCTGGGTTCTGTATTTCACTTCTTTCGATACGGCTTAGGGTAATGTGAGTACAGGAAAAAACTGTGCAA
64 GTGAGCACCTGAT
65 >3325591H1 PTHYN0T03 INCYTE
66 TGCAACAGCTCTTTTGAGAGGAGGCCCTAAAGGACAGGAGAAAAGCTTCAATCGTGGAAAGAAAATTAAATGTTCTATT
67 AAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCTAGCTGGGTTCTGTATTTCAGTTCTTTTCGATACG
68 GCTTAGGGTAATGTGAGTACAGGAAAAAACTGTGCAAGTGAGCACCTGATTCCGTTGCTTGAACCTTAAAGCNC
69 ATGTCNNGGGCNAAAAACGAAAAAT
70 >3733565H1 SYCCN0S01 INCYTE
71 CCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCATCTTCAGGATTACAGTGCATTCTGNAAGANGAGACATCAAAACAG
72 AATTAGGNGTTGTGCAAAAGCTCTTTTGAGAGGAGGCCCTAAAGGACAGGAGAAAAGCTCTNCAATCGTGGAAAGNAAT
73 AAATCTTGTATNAATNGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCTAGCTGGGNCNGTATTACGCT
74 TTTGGAACGGCTTAGGGTAATGTGTCAGTACAOGANAAAACTGTGTCAGTGAG
75 >3554223H1 SYNONOT01 INCYTE

Fig 14

76 ATTAAATAGATCACCAGCTTTTCAGAGTTACCATGTACGTATTCCACTAGCTTCTGTATTTCACTTCTTTTCGAT
 77 ACGGCTTAGGGTAATGTCAACAGGAAAAAACTGTGCAAGTGAGCACCTGATTCGCTTGGCTTAACTCTAAAG
 78 CTCCATGTCTCTGGGCCTAAAATCGTATAAATCTCGATTTTTTTTTTTTTTTTTATATTACATATGTAAACCAGN
 79 ACATTCTATGTACNACAAACCTCGTTTTTAAAAAGQAAC
 80 >4507477H1 OVAR101 INCYTE
 81 CCTAGTTTCAGACTTACCATGTACGTATTCCACTAGCTGGGTTCTGTATTTCACTTCTTTTCGATACGGCTTAGGCTAAT
 82 CTCAGTACAGGAAAAAACTGTGCAAGTGAGCACCTGATTCCTTGCCTTAACTCTAAAGCTCCATGTCTTGGCCC
 83 TAAAATCGTATAAATCTGGA
 84 >4163378H1 BRSTNOT32 INCYTE
 85 AATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGNTCTGTATTTCACTTCTTTTCGATACG
 86 GCTTAGGGTAATGTCACTACAGGAAAAAGCTGTGCAAGTGAGCACCTGATTCCTTGCCTTAACTCTAAAGCTCC
 87 ATGTCCTGGCCCTAAAATCCTATA

Fig 14 (cont'd)

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Fig. 15 (cont.)

76 >877279H1 LUNG1ST01 INCYTE
77 CTTTTTATGACAACCTTAACTATTTTAGCTTGGTAAATTTTCTAAAC TGTATAGCCAGAGGAACAAA
78 GATGATATAAAATATTGTGCTCTCAAAAAATACATGTATTTCATTCTCGTATG TAGAGTTAGATTAACTCGCAT
79 TTTAAAAAACTCAATTGGAATAGAAATGGTAAAGTTCGAAAGGCTTTTGAATAATTAATATCATATCTTCCATTCC
80 TGTATTGGNGG
81 >4713188H1 BRAINCT01 INCYTE
82 CAAAGCTTACTAAAAAATACCACGAGCTCCTTCAGTTCAGACCAAAGACCGGTGTCAGGGGATTGCCACAAATCACATCACCC
83 ACGTGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGTGCAGAGGGAGCACAGGAGGATAGCCGCATCACCACCAGCG
84 CTCTTGGCCAGAGCTGTGTGAGTGCAGTGTGCTGATTCTATTAGAGAACGATGCGTTATCTCCATCCTTAATCTCAGTTGT
85 TTGCT
86 >2171082H1 ENDCNOT03 INCYTE
87 AGATAAACCTGAAAAGAAGAGTGGCCTTATCTTCACTTTATCGATAAGTCAGTTTATTTGTTTCATTOTGTACATTTTAA
88 TATTCTCCTTTTGACATTATAAAGTGTGGCTTTTCTAATCTTGTAAATATATCTATTTTACCAGAGGTATTTAATATT
89 CTTTTTATGACAACCTTAGATCAACTATTTTAGCTTGGTAAATTTTCTAAACACAATTGTATAGCCAGAGGAACAAA
90 GATGA
91 >875860H1 LUNGAST01 INCYTE
92 CTGGATTTTTCATATTCTTATTAAAAATTTCTGCCATTTAGAGAAGAGAACTACATTCATGGTTTGAAGAGATAAACC
93 TGAAAAGAAGAGTGGCCTTATCTTCACTTTATCGATAAGTCAGTTTATTTGTTTCATTGTGTACATTTTATATTCTCCT
94 TTTGACATTATAAAGTGTGGCTTTCTAATCTTGTATAATATATCTATTTTTACCAGAGGTATTTAATATTCTTTTAT
95 GAC
96 >706168H1 SYNORAT04 INCYTE
97 GCTCATATTCACATATGTAAACCAGAACATTCTATOTACTACAAACCTGGTTTTTAAAAAGGANCATGTTGCTATGAAT
98 TAAACTTGTGTCGTCTGATAGSACAGACTGGATTTTTCATATTTCTTATTAAAAATTTCTGCCATTTAGAAGAAGAGAAC
99 TACATTCATGGTTTGAAGAGATAAACCTGAAAAGAAGAGTGGCCTTATCTTCANTTTATCGATAAGTCAGTTTATTGT
100 TTCA
101 >459223H1 KERPNOT01 INCYTE
102 ANGAGTTGCCAGAGCTGTSCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCATCCTTAATCTCAGTT
103 GTTGNNTTCAAGGACCTTTTCACTTCAGGATTACAGTGCATTCTGAAAAGAGAGACATCAACAGAAATAGGAGTTGTG
104 CAAAGCTCTTTTGACAGGAGGCTTAAAGGNCAGGAGAAAAGGCTCTTCAATCGTGAAGAAAATTAATGTTGTATTAA
105 ATAGATC
106 >538436H1 LNCN0T02 INCYTE
107 AAAGATGATATAAAATATTGTTGCTCTGACAAAAATACATGTATTTTCATTCTCGTATGGTGTAGAGTTAGATTAACTG
108 CATTTTAAAAAAGTGAATTGGAATAGAATTGGTAAAGTTGCAAGACTTTTGAAGAAATTAATAATTAATCATATCTTCCAT
109 TCCTGTTATTGGAGATGAAAATAAAAGCAACTTATGAAAGTAGACATTCAGATCCAGCCATTACTAACCTAT
110 >1303909H1 FLACNOT01 INCYTE
111 AGGAAATCAAAATTAGGATAAAGATTGTATCTGATGAATATTTTCTTCTGAACTTCTAACAGAGGAGGTAAAGATTATAC
112 AGCTGCACACCTCGTAACCTCTCAGTGTCCATAAGGGAGAAGTAAAGAGAACCGATACCATTCTTGGCCAGGTTGTCT
113 CCTGTTAAACGCTGTGGTGGGAAGCTGTGCTGCTTCCACAATTCGAATGAATGTCAATGTGTGCCAAG
114 >2739211H1 OVARNOT09 INCYTE
115 GTGCAATCTGAAGAGGAGACATCAACAGAAATAGGAGTGTGTGCAACAGCTCTTTTGAGAGGAGGCCTAAAGGACAGGA
116 GAAAAGGTCTTCAATCTGTGGAAGGAAAATTAATGTTGTATTAAATAGATCACCAGCTAGTTTCAAGATTACCATGTACG
117 TATTCACCTAGCTGGGTTCTGTATTTCAGTTCTTTGATACGGCTTAGGGTAATGTCAATGTGTGCCAAG
118 GTGAGCACCTGAT
119 >2550343H1 LUNGUT06 INCYTE
120 TGTACATTTTATATTTCTCTTTTGACATTATAACGTTTGCTTTTTCNAATCTTGTAAATATATCTATTTTACCAGG
121 GTATTTAATATTCTTTTATGACAACTTAGATCAACTATTTTTAGCTTGTAAATTTTCTAAACACAATTGTTATAGC
122 CAGAGGAACAAAGATGATATAAAATATTGTGCTCTGACAAAAATACATGTATTTCACTCTCGTATGGTGCTA
123 >5321148H1 PBPFEZ06 INCYTE
124 CACAATTGTATAGCCAGAGGAACAAAGATGATATAAAATATTGTTGCTCTGNCAAAAATACATGTATTTTCACTCTCGTA
125 TGGTGTAGAGTTAGATTAACTGCACTTTTAAAAAAGTGAATTGGAATAGAATTGGTAAAGTTGCAAGACTTTTGAAGA
126 TAATTAATATCATATCTTCCATTCTGTTATTGGAGATGAAATAAAAGCAACTTATGAAAGTAAATTCAGATCCAC
127 CATTACTAAC
128 >879495H1 THYRNOT02 INCYTE
129 ATTTTCATTCTCGTATGGTGTAGAGTTAGATTAACTGCACTTTTAAAAAAGTGAATTGGAATAGAATTGGTAAAGTTGCA
130 AGACTTTTGAAGATAATTAATATATATCTTCCATTCTGTTATTGGAGATGAAAATAAAAGCAACTTATGAAGT
131 AGACATTGATCTCAGCCATTACTAACCTATTCCTTTTTTGGGGAATCTGAGCCTAGCTCAGAAAAACATAAAGCACCT
132 TGAAGAA
133 >3325591H1 PTHYN0T03 INCYTE
134 TGCAACAGCTCTTTTGAGAGGAGGCTTAAAGGACAGGAGAAAAGGCTCTTCAATCGTGAAGAGAAAATTAATGTTGTATT
135 AAATAGATCACCAGCTAGTTTTCAGAGTTACCATGTACGTATTCCACTAGCTGGTTCGTATTTCAGTTCTTCCATACG
136 GCTTAGGCTAATGTCACTACAGGAAAAAAGCTGTGCAAGTGAGCACCTGATTCGTTGCTCTGCTTAACCTTAAAGCNC
137 ATGTCNNNGGCNAAAANCAGAAAT
138 >543890H1 OVARNOT02 INCYTE
139 TTTCTAAACACAATTGTTATAGCCAGAGGAACAAAGATGATATAAAATATTGTTGCTCTGACAAAAATACATGTATTCA
140 TTCTCGTATGGTCTAGTATTAGATTAACTGTCATTTTAAAAAAGTGAATTGGAATAGAATTGGTAAAGTTGCAAGACTTT
141 TTTGAAATAATTAATATCATATCTTCCATTCTGTTATTGGAGGATGAAAATAAAAGCAACTTATGGAAGTATG
142 ACATTGATC
143 >3733565H1 SMCCN0S01 INCYTE
144 CCTTAATCTCAGTTCTTTGCTTCAAGGACCTTTTCATCTTCAGGATTACAGTGCATTCTGNAACANAGACATCAACAG
145 AATTAGGNTTGTGCAAAAGCTCTTTTGAGAGGAGGCTTAAAGGACAGGAGAAAAGGCTTNCATCTGTTGGAAGNAAT
146 AATGTTGTATTAATGATCAGCTAGCTTTCAGACTTACCATGTACCTATTCCTACTACCTGGGNCNGTATTTCAGTCT
147 TCCGGAACCCCTTAGGGTAATGTCACTACAGGANAAGAACTGTGCAAGTGA
148 >4641939H1 PROSTM03 INCYTE
149 GTACTACAAACCTGCTTTTAAAAAGCACTATGTTGCTATGAATTAAGTTGTGTCATGCTGATAGGACAGACTGGAT
150 TTTNCATATTTCTATAAAAAATCTCTCCATTAGAGAGAGAGAACTACATTCATGTTTGGNAGAGATAAACCTGAAAA

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226 CTTTTTAAAAAC TGANTT ATAGANTTCTAAGTTGCAAAGNCNTTTGAAA TTAAGTTATCAGAT
 227 >3530274H1 BLA T09 INCYTE
 228 TTCCATTCCCTGTTATTGGAGATGAAAATAAAAGCAACTTATGAAAGTAGACATT ATCCAGCCATTACTAACCTATT
 229 CCTTTTTTGGGGAAATCTGAGCCTAGCTCAGAAAAACATAAAGCACCTTGAAAAAGACTTGGCAGCTTCCTGATAAAGCG
 230 TGCTGTGCTGTGCAAGTAGGAACACATCCTATTTATTGTGATGTTGTGCTTTTATTATCTAAACTCTGTTCCATACACTTG
 231 TATAAATACATGGATATTTTTTATGTACAGAAGTATGCTCTTTAACCAGTTCA
 232 >3530249H1 BLA T09 INCYTE
 233 CTTCCATTCCCTGTTATTGGAGATGAAAATAAAAGCAACTTATGAAAGTAGACATT ATCCAGCCATTACTAACCTATT
 234 TCCTTTTTTGGGGAAATCTGAGCCTAGCTCAGAAAAACATAAAGCACCTTGAAAAAGACTTGGCAGCTTCCTGATAAAGCG
 235 GTGCTGTGCTGTGCAAGTAGGAACACATCCTATTTATTGTGATGTTGTGCTTTTATTATCTAAACTCTGTTCCATACACT
 236 TGTATAAATACATGGATATTTTTTATGTACAGAAGTATGCTCTTTAACCAGTTCACTTATTCTACCTGG
 237

Fig 15 (cont'd)

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VEGFE1	AAAATGTATGGATACAACTTAC	22
VEGFE2	GTTTGATGAAAGATTGGGCTTG	23
VEGFE3	TTTCTAAAGGAAATCAAATTAG	22
VEGFE4	GATAAGATTGTATCTGATG	20
VEGFE5	GATGTCTCCTCTTTCAG	17
VEGFE6	GCACAACTCCTAATTCTG	18
VEGFE7	AGCACCTGATTCCGTTGC	19
VEGFE8	TAGTACATAGAATGTTCTGG	20
VEGFE9	AAGAGACATACTTCTGTAC	19
VEGFE10	CCAGGTACAATAAGTGAAGTGA	21

Fig. 16

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+3 M N I F L L N L L T E E V R L Y
1 AGGAATCAA ATTAGGATAA GATTGTATC TGATGAATAT TTCCCTCTG AACCTTCTAA CAGAGGAGGT AAGATTATAC
TCCTTTAGTT TAATCCTATT CTAACATAG ACTACTTATA AAAGGAACAC TTGGAAGATT GTCTCCTCCA TTCTAATATG
+3 S C T P R N P S V S I R E E L K R T D T I F W P G C L
81 AGCTGCACAC CTCGTAACCT CTCAGTGTC ATAAGGGAAG AACTAAAGAG AACCCATACC ATTTCTGGC CAGGTTGTCT
TCGACGTGTG GAGCATTGAA GAGTCACAGG TATTCCTTC TTGATTCTC TTGGCTATGG TAAAGACCG GTCCAACAGA
-2
+3 L V K R C G G N C A C C L H N C N E C Q C V P S K V
161 CCTGGTTAAA CGCTGTGGTG GGAAGTGTG CTGTTGTCTC CACAATTCCA ATGAATGTCA ATGTGTCCCA AGCAAAGTAA
GACCAATTT GGCACACCAC CCTTGACAGC GACAAACAGG GTGTTAAGCT TACTTACAGT TACACAGGCT TCGTTTCAAT
-2
+3 T K K Y H E V L Q L R P K T G V R G L H K S L T D V A
+1 V S G D C T N H S P T W P
241 CTAAAAATA CCACGAGGTC CTTCACTTGA GACCAACAGC CGGTGTGAGG GGATTGCACA AATCACTCAC CGACGTGGCC
GATTTTAT GGTGCTCCAG GAAGTCAACT CTGTTTCTG GCCACAGTCC CTAACGTGT TTAGTGAGTG GCTGCACCG
-2
+3 L E H H E E C D C V C R G S T G G
+2 V Q P E H R R I A A S P P A A L A
+1 W S T M R S V T V C A Z G A Q E D S R I T T S S S C
321 CTGGAGCACC ATGAGGAGTG TGACTGTGTG TGCAGAGGCA GCACAGGAGG ATAGCCGCAT CACCACCAGC AGCTCTTGGC
GACCTCGTGG TACTCTCAC ACTGACACAC ACGTCTCCCT CGGTCTCTC TATCGCGTA GTGGTGTG TCCAGAACG
+2 Q S C A V Q W L I L L E N V C V I S I L N L S C L L Q
+1 P E L C S A V A D S I R E R M R Y L H P
401 CAGAGCTGTG CAGTGCAGTG GCTGATTCTA TTAGAGAAGC TATGCGTTAT CTCCATCCTT AATCTCAGTT GTTGTCTTCA
GTCTCGACAC GTCACGTGAC CGACTAAGAT AATCTCTTGC ATACCCAATA GAGGTAGGAA TTAGATCAA CAACGAAGT
+2 G P F I F R I Y S A F
481 AGGACGTTTC ATCTTCAGGA TTTACAGTGC ATTCTGAAAG AGGAGACATC AACAGAATT AGGAGTTGTG CAACAGCTCT
TCCTGGAAAG TAGAAGTCCT AAATGTCAGG TAAGACTTTC TCCTCTGTAG TTGTCTTAA TCCTCAACAC GTTGTGAGA
561 TTTGAGAGGA CGCTAAAGG ACAGGAGAAA AGGTCTTCAA TCGTGGAAAG AAAATTAAAT GTTGTATTAA ATAGATCACC
AAACTCTCTT CCGGATTTC TGTCTCTTTC TCCAGAAATT AGCACCTTTC TTTAATTAA CAACATAATT TATCTAGTGG
641 AGCTAGTTTC AGAGTTACCA TGACGTATT CCACTAGCTG GGTCTGTAT TTCAGTTCTT TCGATACGGC TTAGGGTAAT
TCGATCAAAG TCTCAATGGT ACATGCATAA GGTGATCGAC CCAAGACATA AAGTCAAGAA AGCTATGCCG AATCCATTA
721 GTCAGTACAG GAAAAAACT GTCAAGTGA GCACCTGATT CCGTTGCCCT GGCTTAACTC TAAAGCTCCA TGTCTCGGC
CAGTCATGTC CTTTTTTTGA CAGTTTCACT CGTGGACTAA GGCAACGGAA CCGAATTGAG ATTTCAGGT ACAGGACCGG
801 CTAAAAATCGT ATAAAAATCTG GA
GATTTTAGCA TATTTTAGAC CT

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Fig 17

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+3      M N I F L L N L L T E E V R L Y
1  AGGAAATCAA ATTAGGATAA GATTGTATC TGATGAATAT TTTCCTTCTG AACCTTCTAA CAGAGGAGGT AAGATTATAC
   TCCTTTAGTT TAATCCTATT CTAAACATAG ACTACTTATA AAAGGAAGAC TTGCAACATT GTCTCCTCCA TTCTAATATG
+3  S C T P R N F S V S I R E E L K R T D T I F W P G C L
81  AGCTGCACAC CTCGTAACCT CTCAGTGTCC ATAAGGGAAG AACTAAGAG AACCGATACC ATTTTCTGGC CAGGTGTCT
   TCGACGTGTG GAGCATTGAA GAGTCACAGG TATTCCTTC TTGATTCTC TTGGCTATGG TAAAGACCG GTCCAACAGA
-2
+3  L V K R C G G N C A C C L H N C N E C Q C V P S K V
161 CCTGGTTAAA CGCTGTGGTG GGAAGTGTG CTGTGTGTCT CACAATTGCA ATGAATGTCA ATGTGTCCCA AGCAAAGTTA
   GGACCAATTT GCGACACCAC CTTGACACG GACAACAGAG GTGTAAACCT TACTTACAGT TACACAGGGT TCGTTTCAAT
-2
+3  T K K Y H E V L Q L R P X T G V R G L R K S L T D V A
+1      V S G D C T N H S P T W P
241 CTAAAAATA CCACGAGCTC CTTCACTGA GACCAAAGAC CGGTGTCAGG GGATTGCACA AATCACTCAC CGACGTGCCC
   GATTTTMTAT GGTGTCTCCAG GAACTCACT CTGTTTCTG CCCACAGTCC CCTAAGTGT TTAGTGAGTG GCTGCACCGG
-2
+3  L E H H E E C D C V C R G S T G G
+1      V Q R E H R R I A A S P P A A L A
321 CTGGAGCACC ATGAGGAGTG TGACTGTGTG TGCAGAGGGA GCACAGGAGG ATAGCCGCA? CACCACCAGC AGCTCTTCCC
   GACCTCGTGG TACTCTTCAC ACTEACACAC ACGTCTCCCT CCGTCTCTCC TATCGGCGTA GTGTGGTGGT TCGAGAACCG
-2  Q S C A V Q W L I L L E N V C V I S I L N L S C L L Q
+1  P B L C S A V A D S I R E R M R Y L H P
401 CAGAGCTGTG CAGTGCAGTG CCGTATTCTA TTAGAGAAGC TATGCTTAT CTCCATCCTT AATCTCAGTT GTTGTCTCA
   GTCTCGACAC GTCACGTCAC CGACTAAGAT AATCTCTTGC ATACGCAATA CAGGTAGGAA TTAGAGTCAA CAAACGAAT
+2  G P F I F R I Y S A F
481 AGGACCTTTC ATCTTCAGGA TTTACAGTGC ATTCTGAAG AGGAGACATC AAACAGAATT AGGAGTTGTG CAACAGCTCT
   TCCTGGAAG TAGAAGTCTT AAATCTCAGG TAAGACTTTC TCCTCTGTAG TTGTCTTAA TCCTCAACAC GTTGTCTGAG
561 TTTGACAGGA GGCCTAAAGG ACACGAGAAA AGGTCTTCAA TCGTGGAAG AAAATTAAAT GTTGATTTAA ATAGATCACC
   AACTCTCTCT CCGGATTTC TGTCTCTTT TCCAGAGTT AGCACCTTC TTTTAATTAA CAACATAATT TATCTAGTGG
641 AGCTAGTTTC AGAGTTACCA TGTACGTATT CCACTAGCTG GGTCTGTAT TTCAGTCTT TCGATACGGC TTAGGGTAAT
   TCGATCAAAG TCTCAATGOT ACATGCATAA GGTGATCGAC CCAAGACATA AAGTCAAGAA AGCTATGCCG AATCCCATTA
721 GTCAGTACAC CAAAAAACT GTGCAAGTGA GCACCTGATT CCGTTCCTT GGCTTAACTC TAAACCTCCA TGTCTCTGGC
   CAGTCATGTC CTTTMTTGA CACGTTCACT CCGGACTTAA GGCACCGAA CCGAATTGAG ATTTGAGGT ACAGGACCCG
801 CTAAATCGT ATAAATCTG GATTTTITN TTTTITTTG CGCATATTCA CATATGTAAA CCAGAACATT CTATGTACTA
   GATTTTAGCA TATTTTAGAC CTAAAAAAN AAAAAAAR GCGTATAAGT GTATACATT GTCTTGTAA GATACATGAT
881 CAAACCTGGT TTTTAAAAAG GAATTAAGT GCTATGAATT AAATGTGTG CGTGCTGATA GGACAGACTG GATTTTTCAT
   GTTGGACCA AAAATTTTC GTTGATCAA CGATACTTAA TTTGAACACA GCAGGACTAT CCGTCTGAC CTAAAAAGTA
-3

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Fig 18

961 ATTTCTTATT AAAATTTCTG CCATTAGAA GAAGAGAACT ACATTCATGG TTGGAAGAG ATAAACCTGA AAGAGAGACT
 TAAAGATATA TTTAAAGAC GGTAAATCTT CTCTCTTGA TGTAACTACC AAACCTTCTC TATTGGACT TTTCTTCTCA
 -3 -----
 1041 GGCCTTATCT TCACTTTATC GATAAGTCAG TTTATTTGTT TCATTCTGTA CATTTTATA TTCTCCTTTT GACATTATAA
 CCGGATAGA AGTGAATAG CTATTTCAGTC AAATAAACAA AGTAACACAT GTAAATATAT AAGAGGAAAA CTGTAATATT
 -3 -----
 1121 CTGTGGCTT TTCTAATCTT GTTAAATATA TCTATTTTAA CCAAGGTAT TTAATATTCT TTTTATGAC AACCTAGATC
 GACAACCGAA AAGATTAGAA CAATTTATAT AGATAAAAT CCTTCCATA AATTATAAGA AAAAATACG TTGAATCTAG
 1201 AACTATTTT AGCTTGTAA ATTTTCTAA ACACAATTCT TATAGCCAG GGAACAAAGA TGATATAAAA TATTGTGCT
 TTGATAAAAA TCGAACCATT TAAAAGATT TGTGTTAACA ATATCGTCT CCTTGTCTT ACTATATTT ATAACAACGA
 1281 CTGACAAAAA TACATGTATT TCATTCTCGT ATGGTGCTAG AGTAGATTA ATCTGCATT TAAAAAAGT AATTGSAATA
 GACTGTTTTT ATGTACATAA AGTAAGAGCA TACCACGATC TCAATCTAAT TAGACGTAAA ATTTTGTGAC TTAACCTTAT
 1361 GAATTGGTAA GTTGCAAGA CTTTGTGAAA ATAATTAAAT TATCATATCT TCCATTCTCTG TTATTGGAGA TGAAATATAA
 CTTAACCATT CAACGTTTCT GAAAACTTT TATTAATTTA ATAGTATAGA AGCTAAGGAC AATAACCTCT ACTTTTATTT
 1441 AAGCAACTTA TGAAGTAGA CATTGAGATC CAGCCATTAC TAACCTATTC CTTTTTGGG GAAATCTGAG CCTAGCTCAG
 TTGCTGAAT ACTTTCATCT GTAACCTAG CTCGGTAATG AITGCATAAG GAAAAAACC CTTTAGACTC GGATCGAGTC
 1521 AAAACATAA AGCACCTTGA AAAAGACTTG GCAGCTTCTT GATAAAGCGT GCTGTGCTGT GCAGTAGGAA CACATCCTAT
 TTTTGTATT TCGTGAAGT TTTCTGAAC CGTCGAAGGA CTATTTCGCA CGACAGGACA CGTCATCCTT GTGTAGGATA
 1601 TTATGTGAT GTTGTGTTT TATTATCTTA AACTCTGTTT CATACACTTG TATAAATACA TGGATATTT TATGTACAGA
 AATAACACTA CAACACCAA ATAATAGATT TTGAGACAAG GTATGTGAAC ATATTATGT ACCTATATAA ATACATGTCT
 1681 ACTATGCTC TTAACCAGT CACTATTCT ACCTCG
 TCATACAGAG AATTGOTCA GTGAATAACA TGGACC

Fig 18 (cont'd)

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Figure 19. DNA and polypeptide sequence used for mammalian cell expression

+1 m s l f g l l l l t s a l a g g r
 1 GGATCCAAAA TGAGCCTCTT CGGGCTTCTC CTGCTGACAT CTGCCCTGGC CGGCCAGAGA

 +1 q g t q a e s n l s s k f q f s s n k e
 61 CAGGGGACTC AGGCGGAATC CAACCTGAGT AGTAAATTC AGTTTCCAG CAACAAGGAA

 +1 Q N G V Q D P Q H E R I I T V S T N G S
 121 CAGAACGGAG TACAAGATCC TCAGCATGAG AGAATTATTA CTGTGTCTAC TAATGGAAGT

 +1 I H S P R F P H T Y P R N T V L V W R L
 181 ATTCACAGCC CAAGGTTTCC TCATACTTAT CCAAGAAATA CGGTCTTGGT ATGGAGATTA

 +1 V A V E E N V W I Q L T F D E R F G L E
 241 GTAGCAGTAG AGGAAAATGT ATGGATACAA CTTACGTTTG ATGAAAGATT TGGGCTTGAA

 +1 D P E D D I C K Y D F V E V E E P S D G
 301 GACCCAGAAG ATGACATATG CAAGTATGAT TTTGTAGAAG TTGAGGAACC CAGTGATGGA

 +1 T I L G R W C G S G T V P G K Q I S K G
 361 ACTATATTAG GGCCTGGTG TGGTCTGGT ACTGTACCAG GAAAACAGAT TTCTAAAGGA

 +1 N Q I R I R F V S D E Y F P S E P G F C
 421 AATCAAATTA GGATAAGATT TGTATCTGAT GAATATTTTC CTTCTGAACC AGGGTTCTGC

 +1 I H Y N I V M P Q F T E A V S P S V L P
 481 ATCCACTACA ACATTGTCTAT GCCACAATTC ACAGAAGCTG TGAGTCCTTC AGTGCTACCC

 +1 P S A L P L D L L N N A I T A F S T L E
 541 CCTTCAGCTT TGCCACTGGA CCTGCTTAAT AATGCTATAA CTGCCTTTAG TACCTTGGA

 +1 D L I R Y L E P E R W Q L D L E D L Y R
 601 GACCTTATTC GATATCTTGA ACCAGAGAGA TGGCAGTTGG ACTTAGAAGA TCTATATAGG

 +1 P T W Q L L G K A F V F G R K S R V V D
 661 CCAACTGGC AACTTCTTGG CAAGGCTTTT GTTTTGGAA GAAATCCAG AGTGGTGGAT

 +1 L N L L T E E V R L Y S C T P R N F S V
 721 CTGAACCTTC TAACAGAGGA GGTAAAGATTA TACAGCTGCA CACCTCGTAA CTTCTCAGTG

 +1 S I R E E L K R T D T I F W P G C L L V
 781 TCCATAAGGG AAGAACTAAA GAGAACCGAT ACCATTTTCT GGCCAGGTTG TCTCCTGGTT

 +1 K R C G G N C A C C L H N C N E C Q C V
 841 AAACGCTGTG GTGGGAAC TGCTGTGTGT CTCCACAATT GCAATGAATG TCAATGTGTC

 +1 P S K V T K K Y H E V L Q L R P K T G V
 901 CCAAGCAAAG TTAATAAAAA ATACCACGAG GTCCTTCAGT TGAGACCAAA GACCGGTGTC

 +1 R G L H K S L T D V A L E H H E E C D C
 961 AGGGGATTGC ACAAATCACT CACCGACGTG GCCCTGGAGC ACCATGAGGA GTGTGACTGT

 +1 V C R G S T G G S R Q P F E G K P I P N
 1021 GTGTGCAGAG GGAGCACAGG AGGATCTAGA GGGCCCTTCG AAGGTAAGCC TATCCCTAAC

 +1 P L L G L D S T R T C H H H H H H
 1081 CCTCTCCTCG GTCTCGATTG TACGCGTACC GGTATCATC ACCATCACCA TTGA

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Figure 20. DNA and polypeptide sequence used for baculovirus/insect cell expression

1 GAATTCAAAG GCCTGTATTT TACTGTTTTT GTACAGTTT TGTAATAAAA AAACCTATAA
+3 m k f l v n v a l v f m v v y i s y i
61 ATATGAAATT CTTAGTCAAC GTTGCCCTTG TTTTATGGT CGTATACATT TCTTACATCT
+3 Y a D P E S H H H H H E S N L S S K F
121 ATGCGGATCC GSAGTCTCAC CATCACCACC ATCATGAATC CAACCTGAGT AGTAAATTC
+3 Q F S S N K E Q N G V Q D P Q H E R I I
181 AGTTTCCAG CACAAGGAA CAGAACGGAG TACAAGATCC TCAGCATGAG AGAATTATTA
+3 T V S T N G S I H S P R F P H T Y P R N
241 CTGTGTCTAC TAATGGAAGT ATTCACAGCC CAAGGTTTCC TCATACTTAT CCAAGAAATA
+3 T V L V W R L V A V E E N V W I Q L T F
301 CGGTCTTGGT ATGGAGATTA GTAGCAGTAG AGGAAATGT ATGGATACAA CITACGTTTG
+3 D E R F G L E D P E D D I C K Y D F V E
361 ATGAAAGATT TGGGCTTGAA GACCCAGAAG ATGACATATG CAAGTATGAT TTTGTAGAAG
+3 V E E P S D G T I L G R W C G S G T V P
421 TTGAGGAACC CAGTGATGGA ACTATATTAG GCGCGTGGTG TGGTTCTGGT ACTGTACCAG
+3 G K Q I S K G N Q I R I R F V S D E Y F
481 GAAAACAGAT TTCTAAAGGA AATCAAATTA GGATAAGATT TGTATCTGAT GAATATTTTC
+3 P S E P G F C I H Y N I V M P Q F T E A
541 CTTCTGAACC AGGTTCTGTC ATCCACTACA ACATTGTCAT GCCACAATTC ACAGAAGCTG
+3 V S P S V L P P S A L P L D L L N N A I
601 TGAGTCCTTC ATGCTACCC CTTTCAGCTT TGCCACTGGA CCTGCTTAAT AATGCTATAA
+3 T A F S T L E D L I R Y L E P E R W Q L
661 CTGCCTTTAG TACCTTGGA GACCTTATTC GATATCTTGA ACCAGAGAGA TGGCAGTTGG
+3 D L E D L Y R P T W Q L L G K A F V F G
721 ACTTAGAAGA TCTATATAGG CCAACTTGGC AACTTCTTGG CAAGGCTTTT GTTTTGGAA
+3 R K S R V V D L N L L T E E V R L Y S C
781 GAAATCCAG ATGGGTGGAT CTGAACCTTC TAACAGAGGA GGTAAGATTA TACAGCTGCA
+3 T P R N F S V S I R E E L K R T D T I F
841 CACCTCGTAA CTTCTCAGTG TCCATAAGGG AAGAATAAA GAGAACCGAT ACCATTTTCT
+3 W P G C L L V K R C G G N C A C C L H N
901 GGCCAGGTTG TCTCCTGGTT AAACGCTGTG GTGGGAAGTG TGCCTGTTGT CTCCACAATT
+3 C N E C Q C V P S K V T K K Y H E V L Q
961 GCAATGAATG TCAATGTGTC CCAAGCAAAG TTACTAAAAA ATACCACGAG GTCCTTCAGT
+3 L R P K T G V R G L H K S L T D V A L E
1021 TGAGACCAAA GACCGGTGTC AGGGGATTGC ACAATCACT CACCGACGTG GCCCTGGAGC
+3 H H E E C D C V C R G S T G G
1081 ACCATGAGGA GTGTGACTGT GGTGTCAGAG GGAGCACAGG AGGATAGCTC TAGA

Figure 21. DNA and polypeptide sequence used for *E. coli* expression

+3 Q T N S S S N N N N N N N N N L G I
1 CGCAGACTAA TTCGAGCTCG AACAAACAACA ACAATAACAA TAACAACAAC CTCGGGATCG

+3 E G R I S E F E S N L S S K F Q F S S N
61 AGGGAAGGAT TTCAGAATTC GAATCCAACC TGAGTAGTAA ATTCCAGTTT TCCAGCAACA

+3 K E Q N G V Q D P Q H E R I I T V S T N
121 AGGAACAGAA CGGAGTACAA GATCCTCAGC ATGAGAGAAT TATTACTGTG TCTACTAATG

+3 G S I H S P R F P H T Y P R N T V L V W
181 GAAGTATTCA CAGCCCAAGG TTCCTCATA CTTATCCAAG AAATACGGTC TTGGTATGGA

+3 R L V A V E E N V W I Q L T F D E R F G
241 GATTAGTAGC AGTAGAGGAA AATGTATGGA TACAACTTAC GTTTGATGAA AGATTGTGGC

+3 L E D P E D D I C K Y D F V E V E E P S
301 TTGAAGACCC AGAAGATGAC ATATGCAAGT ATGATTTTGT AGAAGTTGAG GAACCCAGTG

+3 D G T I L G R W C G S G T V P G K Q I S
361 ATGGAACATAT ATTAGGGCGC TGGTGTGGTT CTGGTACTGT ACCAGGAAA CAGATTTCTA

+3 K G N Q I R I R F V S D E Y F P S E P G
421 AAGGAAATCA AATTAGGATA AGATTTGTAT CTGATGAATA TTTTCTTCT GAACCAGGGT

+3 F C I H Y N I V M P Q F T E A V S P S V
481 TCTGCATCCA CTACAACATT GTCATGCCAC AATCACAGA AGCTGTGAGT CCTTCAGTGC

+3 L P P S A L P L D L L N N A I T A F S T
541 TACCCCTTC AGCTTTGCCA CTGGACCTGC TTAATAATGC TATAACTGCC TTAGTACCT

+3 L E D L I R Y L E P E R W Q L D L E D L
601 TGGAAGACCT TATTCGATAT CTTGAACCAG AGAGATGGCA GTTGGACTTA GAAGATCTAT

+3 Y R P T W Q L L G K A F V F G R K S R V
661 ATAGGCCAAC TTGGCAACTT CTGGCAAGG CTTTGTGTTT TGGAAGAAAA TCCAGAGTGG

+3 V D L N L L T E E V R L Y S C T P R N F
721 TGGATCTGAA CCTTCTAACA GAGGAGGTAA GATTATACAG CTGCACACCT CGTAACTTCT

+3 S V S I R E E L K R T D T I F W P G C L
781 CAGTGTCCAT AAGGGAAGAA CTAAAGAGAA CCGATACCAT TTTCTGGCCA GGTGTCTCTC

+3 L V K R C G G N C A C C L H N C N E C Q
841 TGTTAAACG CTGIGGTGGG AACTGTGCCT GTTGTCTCCA CAATTGCAAT GAATGTCAAT

+3 C V P S K V T K K Y H E V L Q L R P K T
901 GTGTCCCAAG CAAAGTTACT AAAAAATACC ACGAGGTCCT TCAGTTGAGA CCAAAGACCG

+3 G V R G L H K S L T D V A L E H H E E C
961 GTGTCAGGGG ATTGCACAAA TCACTACCG ACGTGGCCCT GGAGCACCAT GAGGAGTGTG

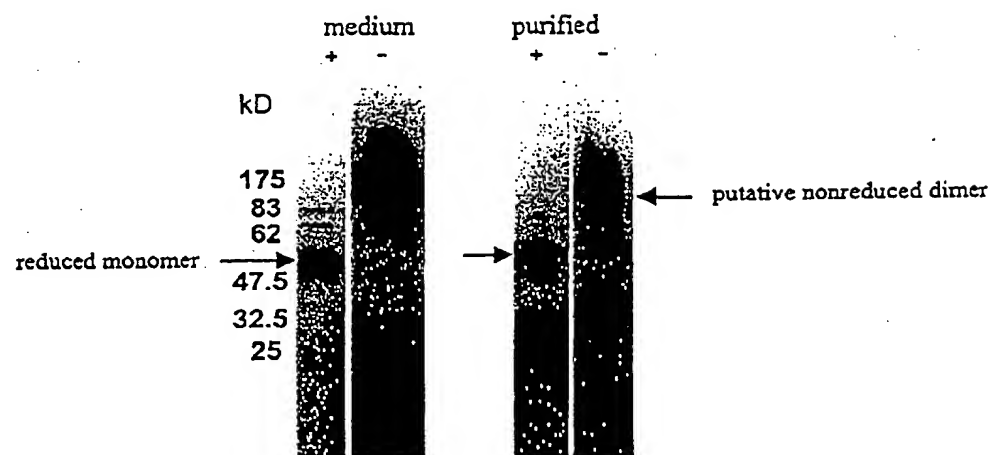
+3 D C V C R G S T G G H H H H H H *
1021 ACTGTGTGTG CAGAGGGAGC ACAGGAGGAC ATCATCACCA TCACCATTGA TCTAGATCG

1081 ACCTGCAGGC AAGCTT

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Figure 22. Disulphide-linked dimerisation of VEGF-X

(A) Mammalian cell expression



(B) *E.coli* expression

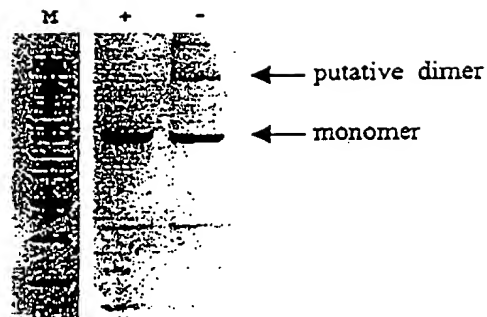


Figure 23. Glycosylation of VEGF-X

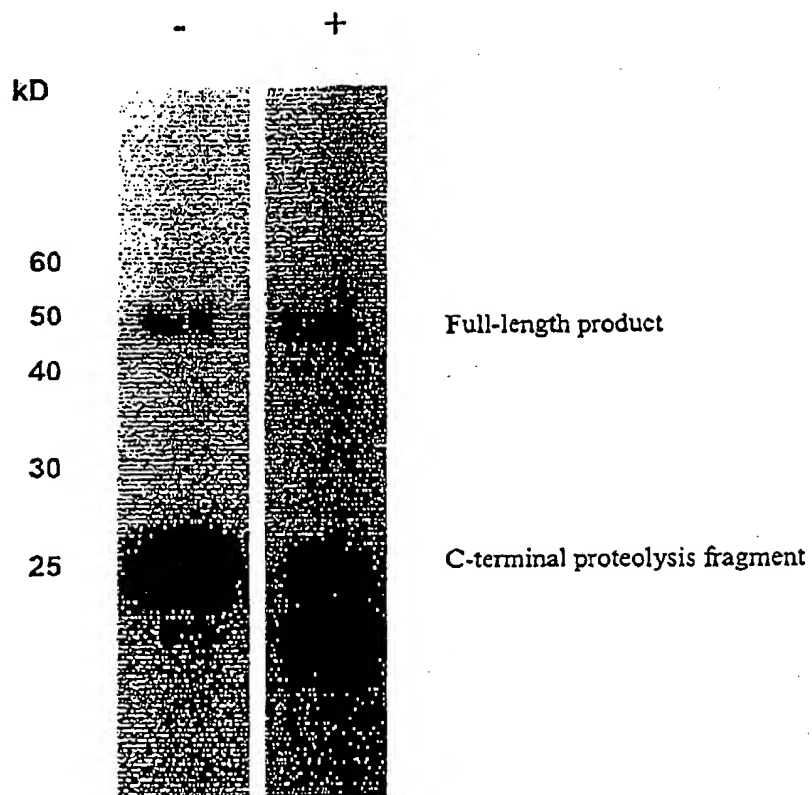


Figure 24. DNA and polypeptide sequence used for *E.coli* expression of the PDGF-like domain

```

+3      M R G S H H H H H H G M A S M
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+3  T G G O O M G R D L Y D D D D K D P G R
61 CTGGTGGACA GCAATGGGT CGGGATCTGT ACGACGATGA CGATAAGGAT CCGGGAAGAA

+3  K S R V V D L N L L T E E V R L Y S C T
121 AATCCAGAGT GGTGGATCTG AACCTTCTAA CAGAGGAGGT AAGATTATAC AGCTGCACAC

+3  P R N F S V S I R E E L K R T D T I F W
181 CTCGTAACCT CTCAGTGTCC ATAAGGGAAG AACTAAAGAG AACCGATACC ATTTTCTGGC

+3  P G C L L V K R C G G N C A C C L H N C
241 CAGGTTGTCT CCTGGTTAAA CGCTGTGGTG GGAAGTGTGC CTGTTGTCTC CACAATTGCA

+3  N E C Q C V P S K V T K K Y H E V L Q L
301 ATGAATGTCA ATGTGTCCCA AGCAAAGTTA CTAAAAATA CCACGAGGTC CTTCASTTGA

+3  R P K T G V R G L H K S L T D V A L E H
361 GACCAAAGAC CGGTGTCAGG GGATTGCACA AATCACTCAC CGACGTGGCC CTGGAGCACC

+3  H E E C D C V C R G S T G G
421 ATGAGGAGTG TGAATGTGTG TGCAGAGGGA GCACAGGAGG ATAATGAATT CGAAGCTTGA

481 TCCGGCTGCT AACAAAGCCC

```

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Figure 25. Expression of PDGF domain in *E.coli*



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Figure 26. DNA and polypeptide sequence used for *E.coli* expression of the CUB-like domain

```

+2   M A M D I G I N S D P E S H H H H H H
1   G G C G A T G G C C A T G G A T A T C G G A A T T A A T T C G G A T C C G G A G T C T C A C C A T C A C C A C C A T C A

+2   E S N L S S K F Q F S S N K E Q N G V Q
61  T G A A T C C A A C C T G A G T A G T A A A T T C C A G T T T T C C A G C A A C A A G G A A C A G A A C G G A G T A C A

+2   D P Q H E R I I T V S T N G S I H S P R
121 A G A T C C T C A G C A T G A G A G A A T T A T T A C T G T G T C T A C T A A T G G A A G T A T T C A C A G C C C A A G

+2   F P H T Y P R N T V L V W R L V A V E E
181 G T T T C C T C A T A C T T A T C C A A G A A T A C G G T C T T G G T A T G G A G A T T A G T A G C A G T A G A G G A

+2   N V W I Q L T F D E R F G L E D P E D D
241 A A A T G T A T G G A T A C A A C T T A C G T T T G A T G A A A G A T T T G G G C T T G A A G A C C C A G A A G A T G A

+2   I C K Y D F V E V E E P S D G T I L G R
301 C A T A T G C A A G T A T G A T T T T G T A G A A G T T G A G G A A C C C A G T G A T G G A A C T A T A T T A G G G C G

+2   W C G S G T V P G K Q I S K G N Q I R I
361 C T G G T G T G G T T C T G G T A C T G T A C C A G G A A A C A G A T T T C T A A A G G A A A T C A A A T T A G G A T

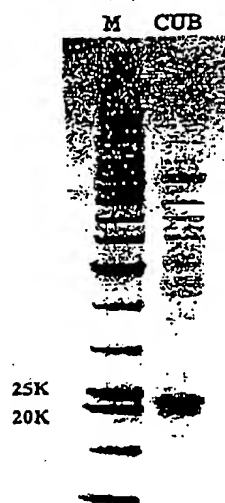
+2   R F V S D E Y F P S E P G F C I H Y N I
421 A A G A T T T G T A T C T G A T G A A T A T T T C C T T C T G A A C C A G G G T T C T G C A T C C A C T A C A A C A T

+2   V M P Q F T E A V
481 T G T C A T G C C A C A A T T C A C A G A A G C T G T G T A G T C G A G C T C C G T C G A C A A G C T T G C G G C C G C

541 A C T C G A G C A C

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Figure 27. Expression of the CUB domain in *E.coli*

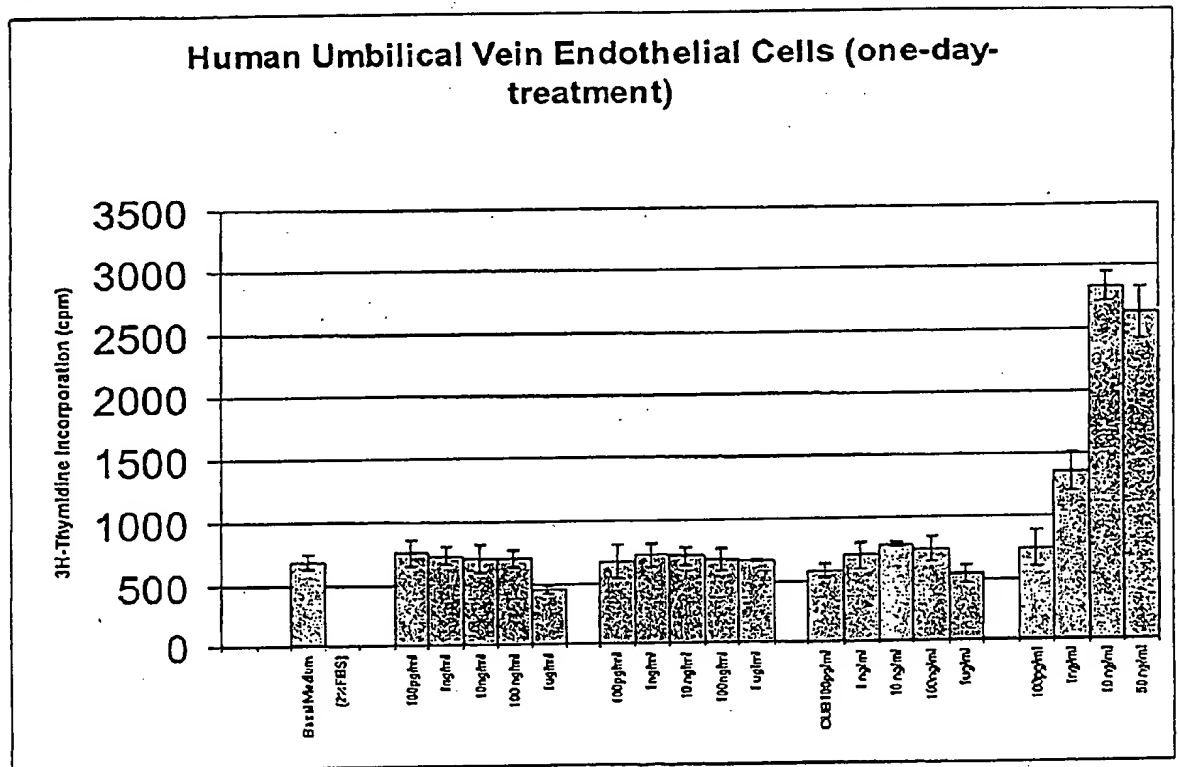


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Figure 28. The Effect of Truncated VEGF-X (CUB domain) on HUVEC Proliferation

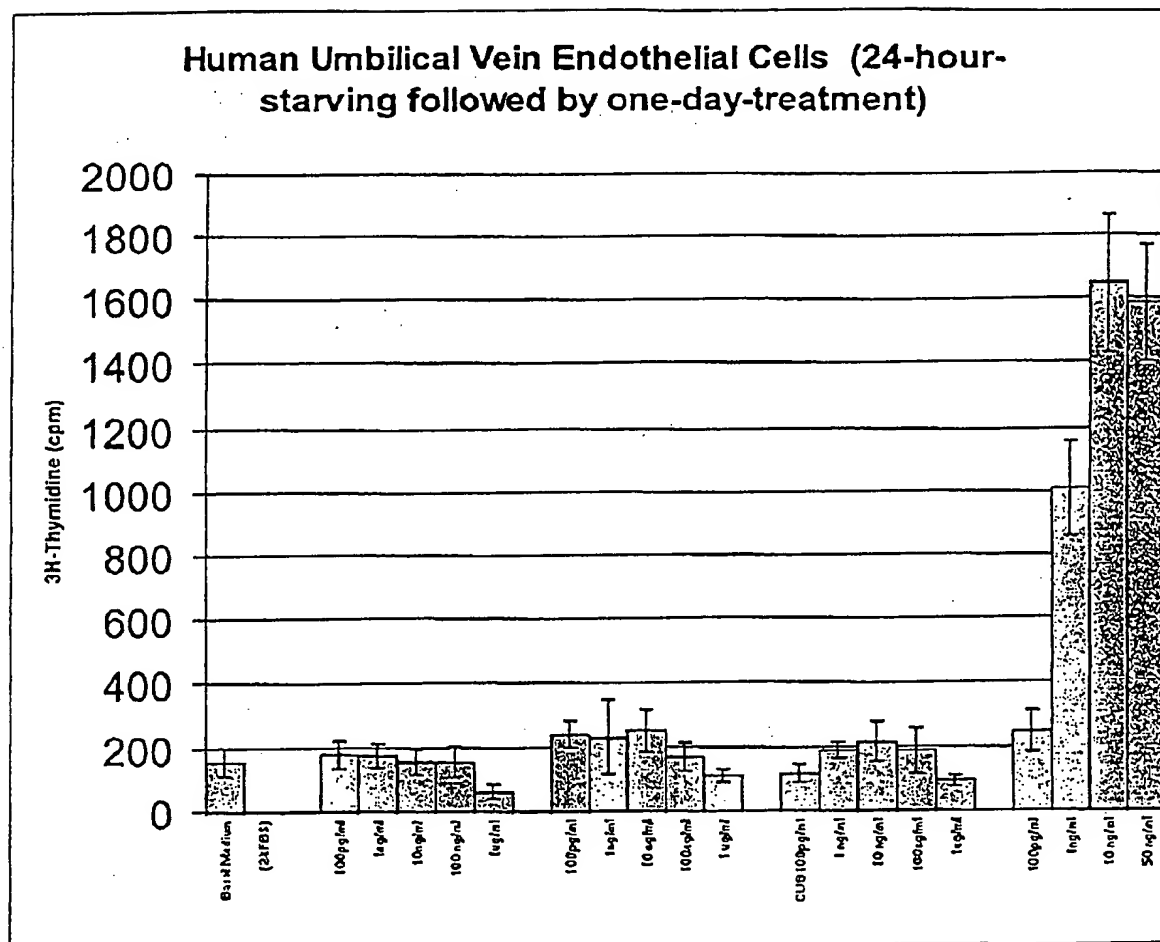
(A)



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Figure 28 Continued

(B)



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Figure 28

(C)- The effect of VEGF-A₁₆₅ and VEGF-X CUB domain on the proliferation of HUVEC (two-day-treatment).

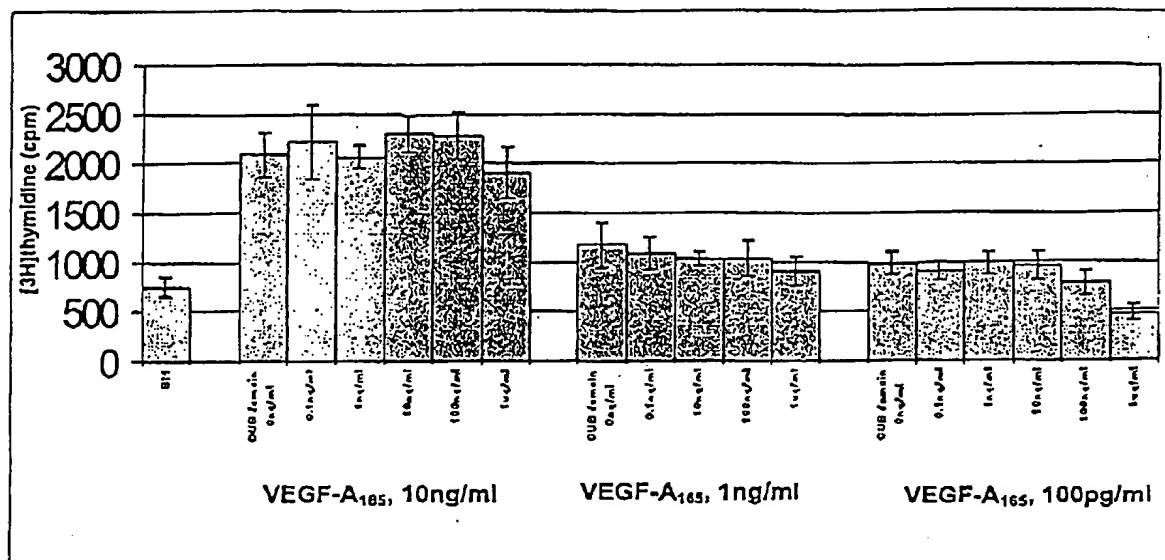
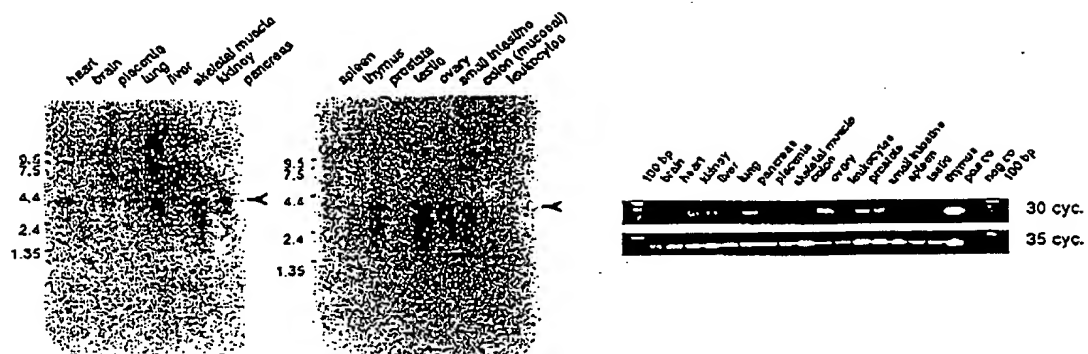


Figure 29 Tissue distribution of mRNA

(A) - Normal tissues



(B) - Tumour tissue and cell lines

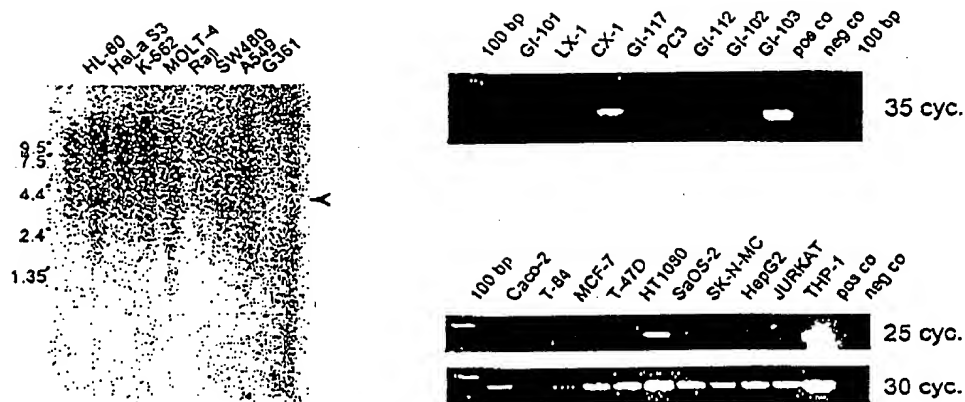


Figure 30. Partial intron/exon structure of the VEGF-X gene

(A) - Genomic DNA sequences of 2 exons determined by sequencing

ttctcttttataccatatagtggtggatctgaaccagGGTTCGTCATCCACTACAACATTGTTCATGCCACAATTCACAGAAGCTGTG
AGTCCTTCAGTGCTACCCCTTCAGCTTTGCCACTGGACCTGCTTAATAATGCTATAACTGCCTTTAGTACCTTGGAAGACCTTAT
TCGATATCTTGAACCAGAGAGATGGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTGT
TTGGAAGAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTATACAGCTGCACACCTCGTAACCTTCTCAGTG
TCCATAAGGGAAGAACTAAAGAGAACCATACCATTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGGTGGGAACCTGTGCTG
TTGTCTCCACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAATACCACGAGtaggtatacaattttctttttt
ggtttctctcggtattttatgtctt

aaagccagtcataagacattcgttgatttttaaagtggcttactcttattccctttcagGTCTTCAGTTGAGACCAAAGACCGGT
GTCAGGGGATTGCACAAATCACTCACCGACGTGGCCCTGGAGCACCATGAGGAGTGTGACTGTGTGTGCAGAGGGAGCACAGGAGG
ATAGCCGCATCACCACCAGCAGCTCTTGCCAGAGCTGTGCAGTGCAGTGGCTGATTCTATTAGAGAACGTATGCGTTATCTCCAT
CCTTAATCTCAGTTGTTTGTCTCAAGGACCTTTTCATCTTCAGGATTTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAAATTAG
GAGTTGTGCAACAGCTCTTTTGAGAGGAGGCCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAAAGAAAATTAAATGTTGTATT
AAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGTTCTGTATTTCAGTTCTTTCCGATACGGCTTAG
GGTAATGTCACTACAGGAAAAAACTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGGCTTAACTCTAAAGCTCCATGTCCTGGGC
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TCGATAAGTCAGTTTATTTGTTTCATTGTGTACATTTTATATTCTCCTTTTGACATTATAACTGTGTCCTTTCTAATCTGTGTTA
AATATATCTATTTTACCAAAGGTATTTAATATCTTTTTTATGACAACTTAGATCAACTATTTTATAGCTTGGTAAATTTTCTAA
ACACAATTGTTATAGCCAGAGGAACAAAGATGATATAAAATATTGTTGCTCTGACAAAAATACATGTATTTCACTTCTCGTATGGTG
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TCATATCTTCATTCTGTTATTGGAGATGAAAATAAAAAGCAACTTATGAAAGTAGACATTAGATCCAGCCATTACTAACCTAT
TCCTTTTTTGGGGAAATCTGAGCCTAGCTCAGAAAAACATAAAGCACCTTGAAAAGACTTGGCAGCTTCTGATAAAGCGTGCTG
TGCTGTGCAGTAGGAACACATCCTATTTATTGTGATGTTGTGGTTTTATTATCTTAACTCTGTTCCATACACTTGATAAATACA
TGGATATTTTATGTACAGAAGTATGTCTCTTAACCAGTTCACTTATTGTAATCTGGCAATTTAAAGAAAATCAGTAAATATTT
TGCTTGTAATATGCTTAATATCGTGCCTAGGTTATGTGGTGACTATTTGAATCAAAAATGTATTGAATCATCAAATAAAGAAATGT
GGCTATTTTGGGGAGAAAATTatgtgtgtgtgtgtcgaagattttattcttggactctgagaaaatgaaagataaa

65T32T 49346

Figure 30 continued

(B) - Location of splice sites within the cDNA sequence

1 GAATTCGCCC TTTTGTAA ACCTTGGGAA CTGTTTCAGG TCCAGGTTTT GCTTTGATCC
61 TTTTCAAAAA CTGGAGACAC AGAAGAGGGC TCTAGGAAAA AGTTTTGGAT GGGATTATGT
121 GGAAACTACC CTGCGATTCT CTGCTGCCAG AGCAGGCTCG GCGCTTCAC CCCAGTGCAG
181 CCTTCCCCTG GCGGTGGTGA AAGAGACTCG GGAGTCGCTG CTTCCAAAGT GCGCGCCGTG
+3 M S L F G L L L L T S
242 AGTGAGCTCT CACCCCAGTC AGCCAAATGA GCCTCTTCGG GCTTCTCCTG CTGACATCTG
+3 A L A G Q R Q G T Q A E S N L S S K F Q
301 CCCTGGCCGG CCAGAGACAG GGGACTCAGG CGGAATCCAA CCTGAGTAGT AAATTCCAGT
+3 F S S N K E Q N G V Q D P Q H E R I I T
361 TTTCCAGCAA CAAGGAACAG AACGGAGTAC AAGATCCTCA GCATGAGAGA ATTATTACTG
+3 V S T N G S I H S P R F P H T Y P R N T
421 TGCTACTAA TGAAGTATT CACAGCCCAA GGTTTCCTCA TACTTATCCA AGAAATACGG
+3 V L V W R L V A V E E N V W I Q L T F D
481 TCTTGGTATG GAGATTAGTA GCAGTAGAGG AAAATGTATG GATACAACCTT ACGTTTGATG
+3 E R F G L E D P E D D I C K Y D F V E V
541 AAAGATTGG GCTTGAAGAC CCAGAAGATG ACATATGCAA GTATGATTTT GTAGAAGTTG
+3 E E P S D G T I L G R W C G S G T V P G
601 AGGAACCCAG TGATGGAACCT ATATTAGGGC GCTGGTGTGG TTCTGGTACT GTACCAGGAA
+3 K Q I S K G N Q I R I R F V S D E Y F P
661 AACAGATTTC TAAAGGAAAT CAAATTAGGA TAAGATTGT ATCTGATGAA TATTTTCCTT
+3 S E P G F C I H Y N I V M P Q F T E A V
721 CTGAACCAAG GTTCTGCATC CACTACAACA TTGTCATGCC ACAATTCACA GAAGCTGTGA
+3 S P S V L P P S A L P L D L L N N A I T
781 GTCCTTCAGT GCTACCCCTC TCAGCTTTC CACTGGACCT GCTTAATAAT GCTATAACTG
+3 A F S T L E D L I R Y L E P E R W Q L D
841 CCTTTAGTAC CTTGGAAGAC CTTATTCGAT ATCTTGAACC AGAGAGATGG CAGTTGGACT
+3 L E D L Y R P T W Q L L G K A F V F G R
901 TAGAAGATCT ATATAGGCCA ACTTGGCAAC TTCTTGGCAA GGCTTTTGT TTTGGAAGAA
+3 K S R V V D L N L L T E E V R L Y S C T
961 AATCCAGAGT GGTGGATCTG AACCTTCTAA CAGAGGAGT AAGATTATAC AGCTGCACAC
+3 P R N F S V S I R E E L K R T D T I F W
1021 CTCGTAACTT CTCAGTGTCC ATAAGGGAAG AACTAAAGAG AACCGATACC ATTTCTGGC
+3 P G C L L V K R C G G N C A C C L H N C
1081 CAGGTGTCT CTTGGTTAAA CGCTGTGGTG GGAAGTGTGC CTGTTGTCTC CACAATTGCA
+3 N E C Q C V P S K V T K K Y H E V L Q L
1141 ATGAATGTCA ATGTGTCCCA AGCAAAGTA CTAATAATA CCACGAGTCT CTCAGTTGA

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 +3 H E E C D C V C R G S T G G
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 1381 CTCCATCCTT AATCTCAGT GTTTGCTTCA AGGACCTTTC ATCTTCAGGA TTTACAGTGC
 1441 ATTCTGAAAG AGGAGACATC AAACAGAATT AGGAGTTGTG CAACAGCTCT TTTGAGAGGA
 1501 GGCCTAAAGG ACAGGAGAAA AGGTCTTCAA TCGTGGAAG AAAATTAAAT GTTGTATTAA
 1561 ATAGATCACC AGCTAGTTTC AGAGTTACCA TGTACGTATT CCACTAGCTG GGTCTGTAT
 1621 TTCAGTTCTT TCGATACGGC TTAGGGTAAT GTCAGTACAG GAAAAAACT GTGCAAGTGA
 1681 GCACCTGATT CCGTTGCCTT GCTTAACTCT AAAGCTCCAT GTCCTGGGCC TAAAATCGTA
 1741 TAAAATCTGG ATTTTTTTT TTTTTTTTG CTCATATTCA CATATGTAAA CCAGAACATT
 1801 CTATGTACTA CAAACCTGGT TTTTAAAAG GAACTATGTT GCTATGAATT AAACCTGTGT
 1861 CATGCTGATA GGACAGACTG GATTTTTCAT ATTTCTTATT AAAATTTCTG CCATTTAGAA
 1921 GAAGAGAACT ACATTCATGG TTTGGAAGAG ATAAACCTGA AAAGAAGAGT GGCCTTATCT
 1981 TCACTTTATC GATAAGTCAG TTTATTGTT TCATTGTGTA CATTTTTATA TTCCTCTTTT
 2041 GACATTATAA CTGTTGGCCT TTCTAATCTT GTTAAATATA TCTATTTTIA CCAAGGTAT
 2101 TTAATATTCT TTTTATGAC AACTTAGATC AACTATTTT AGCTTGGTAA ATTTTCTAA
 2161 ACACAATTGT TATAGCCAGA GGAACAAAGA TGATATAAAA TATTGTTGCT CTGACAAAAA
 2221 TACATGTATT TCATTCTCGT ATGGTGCTAG AGTTAGATTA ATCTGCATT TAAAAAAGT
 2281 AATTGGAATA GAATTGGTAA GTTGCAAAGA CTTTTTGAAA ATAATTAAAT TATCATATCT
 2341 TCCATTCCTG TTATTGGAGA TGAAAATAA AAGCAACTTA TGAAAGTAGA CATTCAGATC
 2401 CAGCCATTAC TAACCTATTC CTTTTTGGG GAAATCTGAG CCTAGCTCAG AAAAACATAA
 2461 AGCACCTTGA AAAAGACTTG GCAGCTTCCT GATAAAGCGT GCTGTGCTGT GCAGTAGGAA
 2521 CACATCCTAT TTATTGTGAT GTTGTGGTTT TATTATCTTA AACTCTGTTC CATACTTG
 2581 TATAAATACA TGGATATTTT TATGTACAGA AGTATGCTC TTAACAGTT CACTTATTGT
 2641 ACCTGGAAGG GCGAATTCTG CAGATATC

Fig. 30 (cont.)

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The Effect of FL-VEGF-X on HUVEC Proliferation: (24-hour serum starvation followed by one day- treatment)

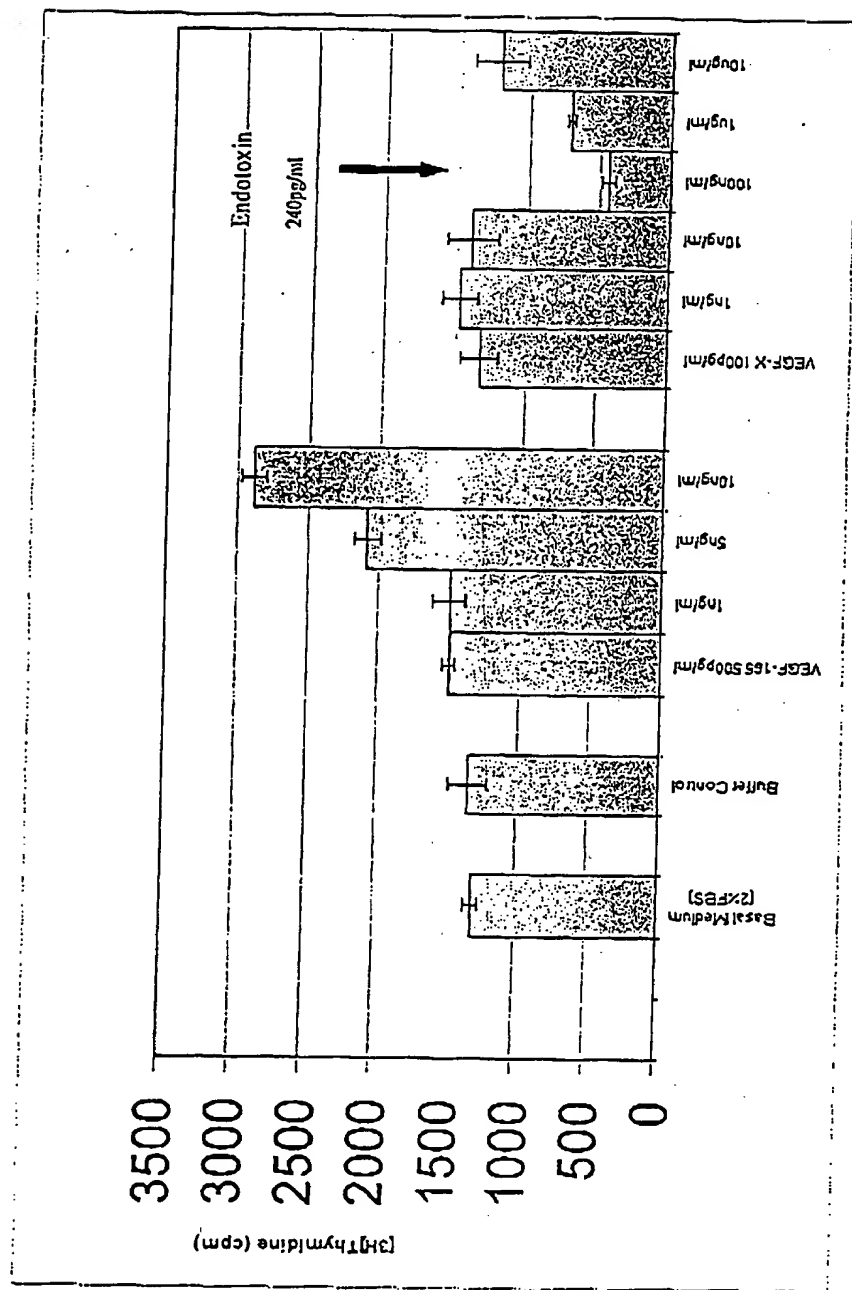


Fig. 31

The Combined Effect of Truncated VEGF-X (CUB domain) and Human Recombinant VEGF₁₆₅ on HUVEC Proliferation: (24-hour serum starvation followed by two-day-treatment)



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The Combined Effect of CUB Domain and Human Recombinant bFGF on HUVEC Proliferation : (24-hour serum starvation followed by two-day-treatment)

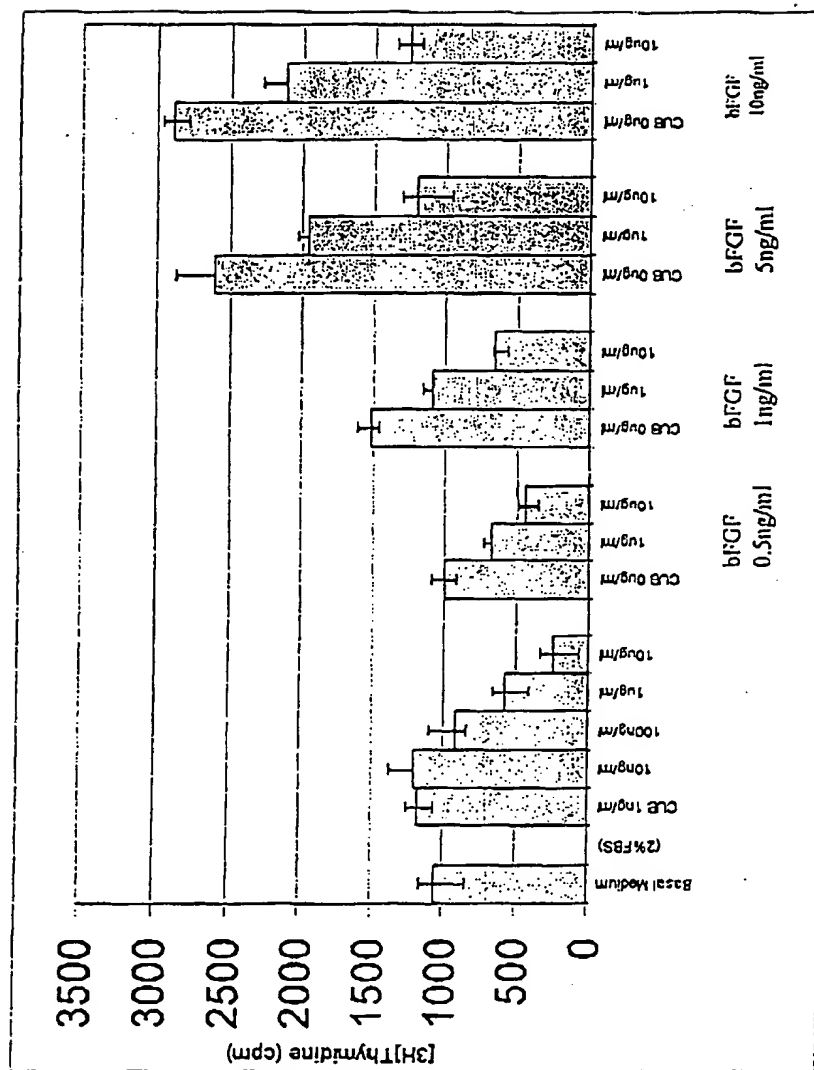
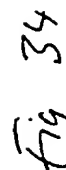


Fig. 33



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LDH Assay for Testing Cytotoxicity of CUB Domain or CUB Domain with rh-bFGF

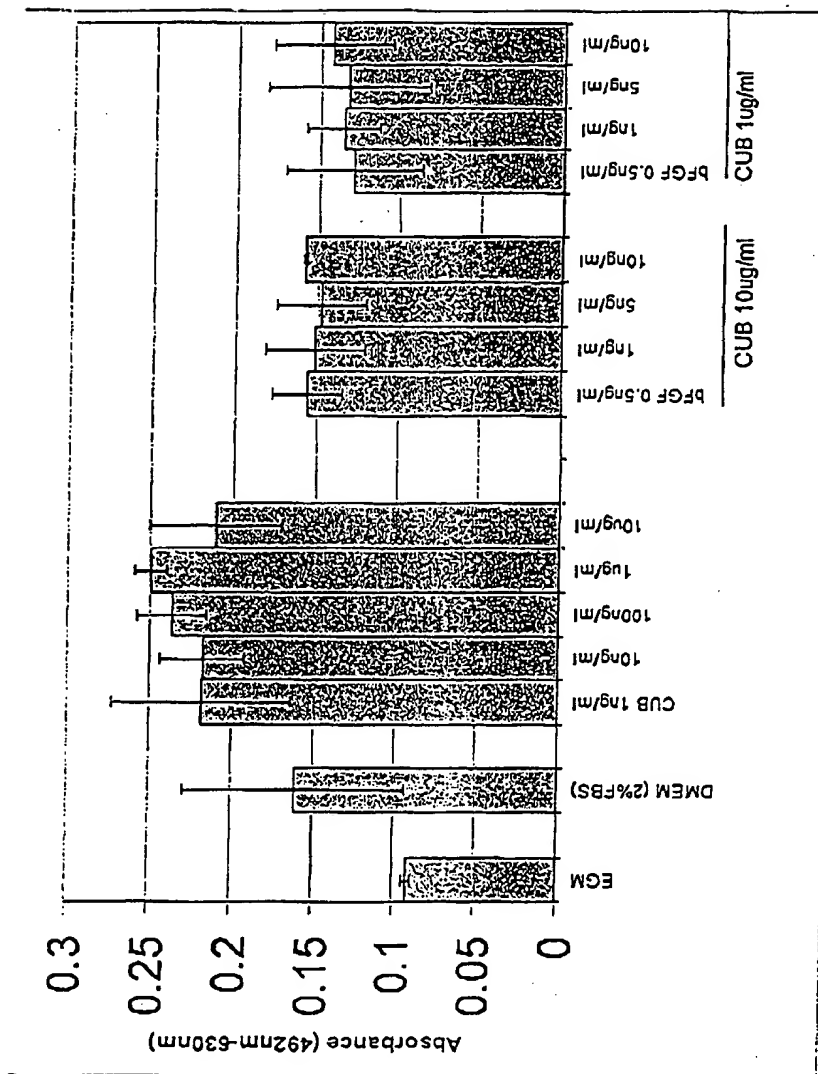


Fig 35

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